

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:24 ; Search time 13.5 Seconds  
(without alignments)  
106.879 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70

Perfect score: 79

Sequence: 1 QNILLSNAPLGPPQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: piri.\*

2: piri2.\*

3: piri3.\*

4: piri4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	529	1 YRHU1	monophenol monooxy
2	67	84.8	273	2 PC4153	monophenol monooxy
3	63	79.7	533	1 YRMSCS	monophenol monooxy
4	49	62.0	532	2 JCI392	monophenol monooxy
5	47	59.5	1708	2 A05205	hypothetical prote
6	47	59.5	2131	2 S01446	hypothetical prote
7	47	59.5	2216	2 S78398	hypothetical prote
8	41.5	52.5	459	2 D70914	hypothetical prote
9	41	51.9	295	2 AB2156	hypothetical prote
10	41	51.9	638	2 AD1166	hypothetical prote
11	41	51.9	662	2 AD0228	probable peptidogl
12	41	51.9	847	1 S36337	neurexin II-beta p
13	41	51.9	1715	2 C40228	histidine decarbox
14	40	50.6	353	1 C54258	neurexin II-alpha
15	40	50.6	354	1 S35090	transcription fact
16	40	50.6	1209	2 TS2523	transcription fact
17	39	49.4	241	2 S58635	hypothetical prote
18	39	49.4	289	2 AD1355	hypothetical prote
19	39	49.4	376	2 AD2724	hypothetical prote
20	39	49.4	376	2 B27724	actin 1 - Trypanos
21	39	49.4	524	2 H69099	actin 2 - Trypanos
22	39	49.4	1014	1 NMICLS	conserved hypotnet
23	39	49.4	1821	2 AG2335	exo-alpha-sialidas
24	39	49.4	1978	2 S77257	hypothetical prote
25	38.5	48.7	322	2 S73795	hypothetical prote
26	38.5	48.7	502	2 A70988	hypothetical prote
27	38.5	48.7	1218	2 JS0069	hypothetical prote
28	38	48.1	59	2 G98141	hypothetical P1 op
29	38	48.1	60	2 I55550	low density lipopr

30	38	48.1	270	2 AB1308	conserved hypotnet
31	38	48.1	270	2 AB1680	conserved hypotnet
32	38	48.1	378	1 ATSY1	actin 1 - soybean
33	38	48.1	466	2 C89820	cysteinyI-trNA syn
34	38	48.1	486	2 T20482	hypothetical prote
35	38	48.1	508	2 A71453	hypothetical prote
36	38	48.1	1113	2 T14260	period protein per
37	38	48.1	1115	2 T13955	myosin-light-chain
38	38	48.1	1906	1 S68235	probable sideropho
39	38	48.1	2201	2 AH0095	conserved hypotnet
40	37.5	47.5	136	2 G69440	conserved hypotnet
41	37.5	47.5	325	2 C83585	conserved hypotnet
42	37	46.8	154	2 AE0445	biotin carboxyl ca
43	37	46.8	195	2 D97357	uncharacterized pr
44	37	46.8	204	2 AB2383	hypothetical prote
45	37	46.8	222	2 D69026	conserved hypotnet

## ALIGNMENTS

## RESULT 1

## YRHU1

monophenol monooxygenase (EC 1.14.18.1) precursor [validated] - human  
N; Alternate names: cresolase; monophenol oxidase; phenolase; tyrosinase  
C; Species: Homo sapiens (man)  
C; Date: 30-Jun-1990 #sequence revision 31-Mar-1993 #text change 08-Dec-2000  
C; Accession: A38444; S07760; A33393; A38718; JI0098; A40957; S04760; A60149; S5-  
R; Giebel, L.B.; Strunk, K.M.; Spritz, R.A.  
Genomics 9, 435-445, 1991  
A; Title: Organization and nucleotide sequences of the human tyrosinase gene and a trunc-  
A; Reference number: A38444; MUID:91236163; PMID:1903356  
A; Accession: A38444  
A; Molecule type: DNA  
A; Residues: 1-529 <GIE>  
A; Cross-references: GB:M63239; GB:M60296; NID:G340033; PIDN:AA61242.1; PID:G340035  
R; Kikuchi, H.; Miura, H.; Yamamoto, H.; Takeuchi, T.; Dei, T.; Watanabe, M.  
Biochem. Biophys. Acta 1009, 283-286, 1989  
A; Title: Characteristic sequences in the upstream region of the human tyrosinase gene.  
A; Reference number: S07760; MUID:90089403; PMID:2480811  
A; Accession: S07760  
A; Molecule type: DNA  
A; Residues: 1-273 <KIK>  
A; Cross-references: EMBL:X16073; NID:G37506; PIDN:CAA34205.1; PID:G37507  
R; Takeda, A.; Tomita, Y.; Okinaga, S.; Tagami, H.; Shibahara, S.  
Biochem. Biophys. Res. Commun. 162, 984-990, 1989  
A; Title: Functional analysis of the cDNA encoding human tyrosinase precursor.  
A; Reference number: A33393; MUID:89351001; PMID:2504160  
A; Accession: A33393  
A; Molecule type: DNA  
A; Residues: 1-32 <TAK>  
A; Cross-references: GB:M27160  
R; Giebel, L.B.; Tripathi, R.K.; Strunk, K.M.; Hanifin, J.M.; Jackson, C.E.; King, R.A.;  
Am. J. Hum. Genet. 48, 1159-1167, 1991  
A; Title: Tyrosinase gene mutations associated with type IB ("yellow") oculocutaneous alb-  
A; Reference number: A38718; MUID:91241133; PMID:1903591  
A; Accession: A38718  
A; Molecule type: DNA  
A; Residues: 274-280; 401-411; 500-509 <G12>  
R; Bouchard, B.; Fuller, B.B.; Vijayaradhi, S.; Houghton, A.N.  
J. Exp. Med. 169, 2029-2042, 1989  
A; Title: Induction of pigmentation in mouse fibroblasts by expression of human tyrosinase  
A; Reference number: JI0098; MUID:89279151; PMID:2499655  
A; Accession: JI0098  
A; Molecule type: mRNA  
A; Residues: 'GR', 'I', '178', 'I', '180-191', 'Y', '193-529 <BOU>  
A; Cross-references: EMBL:X08819; NID:G37508; PIDN:CAA68756.1; PID:G37509  
R; Chintamaneni, C.D.; Halaban, R.; Kobayashi, Y.; Witkop Jr., C.J.; Kwon, B.S.  
Proc. Natl. Acad. Sci. U.S.A. 88, 5272-5276, 1991  
A; Title: A single base insertion in the putative transmembrane domain of the tyrosinase  
A; Reference number: A40957; MUID:91271371; PMID:1711223  
A; Accession: A40957  
A; Molecule type: mRNA

A;Residues: 1-165,'I',167-489,'CPAGRACELAVSSQEKAAAS' <CHI>  
 A;Cross-references: GB:M74314  
 A;Experimental source: albino melanocytes  
 A;Note: mutant protein isolated from patient with tyrosinase-negative oculocutaneous albinism  
 R;Kwon, B.S.; Haq, A.K.; Pomerantz, S.H.; Halaban, R.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 7473-7477, 1987  
 A;Title: Isolation and sequence of a cDNA clone for human tyrosinase that maps at the melanocyte locus  
 A;Reference number: A94185; MUID:88041128; PMID:2823263  
 A;Accession: S04760  
 A;Molecule type: mRNA  
 A;Residues: 'L',2-41,'TGV',46-191,'Y',193-307,'T',309-372,'HVPQT',379-401,'Q',403-494,'H'  
 A;Cross-references: GB:J03581; NID:G340027; PIDN:AAA61241.1; PID:G340028  
 A;Experimental source: normal melanocytes  
 A;Note: the sequence differs from that shown in several regions due to reading frameshift  
 R;Wittbjer, A.; Odh, G.; Rosengren, A.M.; Rosengren, E.; Rorsman, H.  
 Acta Derm. Venereol. 70, 291-294, 1990  
 A;Title: Isolation of soluble tyrosinase from human melanoma cells.  
 A;Reference number: A60149; MUID:91021767; PMID:1977251  
 A;Accession: A60149  
 A;Molecule type: protein  
 A;Residues: 19-23,'X',25-28 <WIT>  
 A;Note: the sequence was determined from a soluble form of the enzyme from melanoma cell  
 A;Accession: B60149  
 A;Molecule type: protein  
 A;Residues: 19-23,'X',25-34,'XX',37-38 <WIT2>  
 A;Note: the sequence was determined from a membrane-bound form of the enzyme from melanoma cell  
 R;Giebel, L.B.; Strunk, K.M.; Spritz, R.A.  
 submitted to the EMBL Data Library, July 1991  
 A;Description: Organization and nucleotide sequences of the human tyrosinase gene and a pseudogene  
 A;Reference number: S53560  
 A;Accession: S53560  
 A;Molecule type: DNA  
 A;Residues: 396-455 <G13>  
 A;Cross-references: EMBL:M63238  
 R;Wittbjer, A.; Dahlbaeck, B.; Odh, G.; Rosengren, A.M.; Rosengren, E.; Rorsman, H.  
 Acta Derm. Venereol. 69, 125-131, 1989  
 A;Title: Isolation of human tyrosinase from cultured melanoma cells.  
 A;Reference number: A60464; MUID:89163645; PMID:2564229  
 A;Accession: A60464  
 A;Molecule type: protein  
 A;Residues: 'L',2-13;19-23,'X',25-34,'XX',37-38 <W12>  
 R;Guo, Z.; Guilfoyle, R.A.; Thiel, A.J.; Wang, R.; Smith, L.M.  
 Nucleic Acids Res. 22, 5456-5465, 1994  
 A;Title: Direct fluorescence analysis of genetic polymorphisms by hybridization with oligonucleotide probes  
 A;Reference number: S53559; MUID:95116340; PMID:7816638  
 A;Contents: annotation  
 C;Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; it reacts in the formation of pigments such as melanins and other polyphenolic compounds  
 C;Genetics:  
 A;Gene: GDB:TYR  
 A;Cross-references: GDB:120476; OMIM:203100  
 A;Map position: 11q21-11q21  
 A;Introns: 273/3; 346/1; 395/2; 456/1  
 C;Superfamily: monophenol monooxygenase  
 C;Keywords: albinism; copper; glycoprotein; melanin biosynthesis; monooxygenase; oxidoreductase  
 F;1-18/Domain: signal sequence #status predicted <SIG>  
 F;19-529/Product: monophenol monooxygenase #status experimental <MAT>  
 F;474-500/Domain: transmembrane #status predicted <TM>  
 F;86.111,161,230,337,371/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;180,202,211/Binding site: copper (His) #status predicted  
 F;363,367,390,420/Binding site: copper (His) #status predicted

Query Match 100.0%; Score 79; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQFP 15  
 |||||  
 DB 56 QNILLSNAPLGPQFP 70  
 |||||

RESULT 2  
 PC4153

monophenol monooxygenase (EC 1.14.18.1) - chicken  
 N;Alternate names: tyrosinase  
 C;Species: Gallus gallus (chicken)  
 C;Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 03-Feb-2003  
 C;Accession: PC4153  
 R;Perguson, C.A.; Kidson, S.H.  
 Gene 169, 191-195, 1996  
 A;Title: Characteristic sequences in the promoter region of the chicken tyrosinase-encoding gene  
 A;Reference number: PC4153; MUID:96194800; PMID:8647445  
 A;Accession: PC4153  
 A;Molecule type: DNA  
 A;Residues: 1-273 <FER>  
 A;Cross-references: GB:L46805; NID:gl146320; PIDN:AB08441.1; PID:gl146321  
 A;Note: The DNA sequence includes the first exon and a part of the first intron  
 C;Comment: this enzyme is the rate-limiting enzyme in pigment biosynthesis.  
 C;Genetics:  
 A;Gene: ctyr4.3  
 C;Keywords: oxidoreductase

Query Match 84.8%; Score 67; DB 2; Length 273;  
 Best Local Similarity 86.7%; Pred. No. 0.00045;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQFP 15  
 |||||  
 DB 56 QNILLSNAPLGPQFP 70  
 |||||

RESULT 3  
 YRMSCS

monophenol monooxygenase (EC 1.14.18.1) precursor [validated] - mouse  
 N;Alternate names: cresolase, monophenol oxidase; phenolase; tyrosinase  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 20-Apr-2000  
 C;Accession: A27711; A60778; A32429; B32429; S01170; S02278; S15753; I49736  
 R;Kwon, B.S.; Wakulchik, M.; Haq, A.K.; Halaban, R.; Kestler, D.  
 Biochem. Biophys. Res. Commun. 153, 1301-1309, 1988  
 A;Title: Sequence analysis of mouse tyrosinase cDNA and the effect of melanotropin on its expression  
 A;Reference number: A27711; MUID:89268910; PMID:3134020  
 A;Accession: A27711  
 A;Molecule type: mRNA  
 A;Residues: 1-533 <KWO>  
 A;Cross-references: GB:M20234; NID:g202247; PIDN:AAA40516.1; PID:g202248  
 A;Experimental source: Cloudman S-91 melanoma cells  
 R;Kwon, B.S.; Haq, A.K.; Wakulchik, M.; Kestler, D.; Barton, D.E.; Francke, U.; Lamoreux, J.  
 Invest. Dermatol. 93, 589-594, 1989  
 A;Title: Isolation, chromosomal mapping, and expression of the mouse tyrosinase gene.  
 A;Reference number: A60778; MUID:90010220; PMID:2507645  
 A;Accession: A60778  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-273 <KW2>  
 A;Experimental source: BALB/c  
 R;Terao, M.; Tabe, L.; Garattini, E.; Sartori, D.; Studer, M.; Mintz, B.  
 Biochem. Biophys. Res. Commun. 159, 848-853, 1989  
 A;Title: Isolation and characterization of variant cDNAs encoding mouse tyrosinase.  
 A;Reference number: A32429; MUID:89193679; PMID:2494997  
 A;Accession: A32429  
 A;Molecule type: mRNA  
 A;Residues: 1-102,'C',104-345,'G',347-533 <TER>  
 A;Cross-references: GB:M24560; NID:g202249; PIDN:AAA40517.1; PID:g202250  
 A;Accession: B32429  
 A;Molecule type: mRNA  
 A;Residues: 1-77;155-345,'G',347-533 <TE2>  
 A;Cross-references: GB:M24560  
 A;Experimental source: B16 melanoma cells  
 R;Mueller, G.; Ruppert, S.; Schmid, E.; Schuetz, G.  
 EMBO J. 7, 2723-2730, 1988  
 A;Title: Functional analysis of alternatively spliced tyrosinase gene transcripts.  
 A;Reference number: S01170; MUID:89030636; PMID:3141148  
 A;Accession: S01170  
 A;Molecule type: mRNA  
 A;Residues: 1-102,'C',104-263,'I',265-345,'G',347-533 <MUE>

A;Cross-references: GB:X12782; NID:g55061; PIDN:CAA31273.1; PID:g55062  
 R;Yamamoto, H.; Takeuchi, S.; Kudo, T.; Makino, K.; Nakata, A.; Shinoda, T.; Takeuchi, T.  
 Jpn. J. Genet. 62, 271-274, 1987  
 A;Title: Cloning and sequencing of mouse tyrosinase cDNA.  
 A;Reference number: S02278  
 A;Accession: S02278  
 A;Molecule type: mRNA  
 A;Residues: 1-102, 'C', 104-263, 'I', 265-345, 'G', 347-448 <YAM>  
 A;Cross-references: EMBL:X12782  
 A;Note: part of this sequence was confirmed by protein sequencing  
 R;Shibahara, S.; Okinaga, S.; Tomita, Y.; Takeda, A.; Yamamoto, H.; Sato, M.; Takeuchi, T.  
 Eur. J. Biochem. 189, 455-461, 1990  
 A;Title: A point mutation in the tyrosinase gene of BALB/c albino mouse causing the cyst  
 A;Reference number: S15753; MUID:90249393; PMID:2110899  
 A;Accession: S15753  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-13 <SHI>  
 A;Cross-references: EMBL:X51743; NID:g55057; PIDN:CAA36033.1; PID:g55058  
 A;Experimental source: strain BALB/c  
 R;Kwon, B.S.; Halaban, R.; Chintamani, C.  
 Biochem. Biophys. Res. Commun. 161, 252-260, 1989  
 A;Title: Molecular basis of mouse Himalayan mutation.  
 A;Reference number: I49736; MUID:89273644; PMID:2567165  
 A;Accession: I49736  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-39, 'I', 41-102, 'C', 104-196, 'Q', 198-345, 'G', 347-419, 'R', 421-533 <RES>  
 A;Cross-references: GB:M26729; NID:g193845; PIDN:AAA37806.1; PID:g309296  
 A;Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; in  
 reactions in the formation of pigments such as melanins and other polyphenolic compound  
 C;Genetics:  
 A;Gene: Tyrl  
 A;Map position: 7  
 C;Superfamily: monophenol monooxygenase  
 C;Keywords: albinism; alternative splicing; copper; glycoprotein; melanin biosynthesis;  
 F.1-18/Domain: signal sequence #status predicted <SIG>  
 F.19-533/Product: monophenol monooxygenase #status predicted <MAT>  
 F.474-497/Domain: transmembrane #status predicted <TM>  
 F.86,111,161,230,337,371/Binding site: carboxydrate (Asn) (covalent) #status predicted  
 Query Match 79.7%; Score 63; DB 1; Length 533;  
 Best Local Similarity 80.0%; Pred. No. 0.005;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGP 15  
 Db 56 QDILLSAPSGP 70  
 RESULT 4  
 JC1392  
 monophenol monooxygenase (EC 1.14.18.1) - Japanese pond frog  
 N;Alternate names: tyrosinase  
 C;Species: Rana nigromaculata (Japanese pond frog)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
 C;Accession: JC1392; I51169  
 R;Takase, M.; Miura, I.; Nakata, A.; Takeuchi, T.; Nishioka, M.  
 Gene 121, 359-363, 1992  
 A;Title: Cloning and sequencing of the cDNA encoding tyrosinase of Japanese pond frog, R  
 A;Reference number: JC1392; MUID:93077054; PMID:1446833  
 A;Accession: JC1392  
 A;Molecule type: mRNA  
 A;Residues: 1-532 <TAK>  
 A;Cross-references: DDBJ:D12514; NID:g222946; PIDN:BA02077.1; PID:g222947  
 R;Miura, I.; Okumoto, H.; Makino, K.; Nakata, A.; Nishioka, M.  
 Jpn. J. Genet. 70, 79-92, 1995  
 A;Title: Analysis of the tyrosinase gene of the Japanese pond frog, Rana nigromaculata:  
 A;Reference number: I51169; MUID:95290234; PMID:7772385  
 A;Accession: I51169  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-9, 'A', 11-277 <MIU>

A;Cross-references: GB:D37779; NID:g809507; PIDN:BA07034.1; PID:g809508  
 C;Superfamily: monophenol monooxygenase  
 C;Keywords: glycoprotein; oxidoreductase; transmembrane protein  
 F.47,90,115,165,234,294,341,360,375/Binding site: carboxydrate (Asn) (covalent) #status  
 Query Match 62.0%; Score 49; DB 2; Length 532;  
 Best Local Similarity 53.3%; Pred. No. 1.4;  
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGP 15  
 Db 60 QDVFSNPFVGAQFP 74  
 RESULT 5  
 A05205  
 hypothetical protein 1708 - common tobacco chloroplast  
 C;Species: chloroplast Nicotiana tabacum (common tobacco)  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 11-Apr-1995  
 C;Accession: A05205  
 R;Sugiura, M.  
 submitted to the EMBL Data Library, August 1986  
 A;Reference number: A00149  
 A;Accession: A05205  
 A;Molecule type: DNA  
 A;Residues: 1-1708 <SUG>  
 A;Experimental source: cv. Bright Yellow 4  
 R;Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Matsubayashi, T.; Za  
 Deno, H.; Kamogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Tohdoh, N.; Si  
 EMBL J. 5, 2043-2049, 1986  
 A;Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene or  
 A;Reference number: A38013  
 A;Contents: annotation; gene organization, sites, features  
 C;Genetics:  
 A;Genome: chloroplast  
 C;Keywords: chloroplast  
 Query Match 59.5%; Score 47; DB 2; Length 1708;  
 Best Local Similarity 66.7%; Pred. No. 13;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGP 12  
 Db 1334 QNVLLSNCPIDP 1345  
 RESULT 6  
 S01446  
 hypothetical protein 2131 - spinach chloroplast  
 C;Species: chloroplast Spinacia oleracea (spinach)  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jul-2000  
 C;Accession: S01446  
 R;Zhou, D.X.; Massenet, O.; Quigley, F.; Marion, M.J.; Moneger, F.; Huber, P.; Mache, R.  
 Curr. Genet. 13, 433-439, 1988  
 A;Title: Characterization of a large inversion in the spinach chloroplast genome relat  
 A;Reference number: S01446; MUID:88295221; PMID:2841033  
 A;Accession: S01446  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-2131 <ZHO>  
 A;Cross-references: EMBL:X07908; NID:g12245; PIDN:CAA30743.1; PID:g12246  
 C;Genetics:  
 A;Genome: chloroplast  
 C;Keywords: chloroplast  
 Query Match 59.5%; Score 47; DB 2; Length 2131;  
 Best Local Similarity 66.7%; Pred. No. 16;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGP 12  
 Db 1742 QNVLLSNCPIDP 1753

RESULT 7  
S78398  
hypothetical protein 2216 - beechdrops plastid  
C:Species: plastid Epifagus virginiana (beechdrops)  
C:Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 05-Jun-1998  
C:Accession: S78398; S78404  
R:Wolfe, K.H.; Morden, C.W.; Ems, S.C.; Palmer, J.D.  
J. Mol. Evol. 35, 304-317, 1992  
A:Title: Rapid evolution of the plastid translational apparatus in a nonphotosynthetic p  
A:Reference number: S78398; MUID:93021155; PMID:1404416  
A:Accession: S78398  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-2216 <WOL>  
A:Cross-references: EMBL:M81884; NID:G336917; PID:G336938  
A:Genetics: G1  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992  
A:Accession: S78404  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-2216 <WOL>  
A:Cross-references: EMBL:M81884; NID:G336917; PID:G336938  
A:Genetics: G2  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992  
C:Genetics: <G1>  
A:Gene: 2216\_a  
A:Genome: plastid  
C:Genetics: <G2>  
A:Gene: 2216\_b  
A:Genome: plastid  
C:Keywords: plastid

Query Match 59.5%; Score 47; DB 2; Length 2216;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNLLSNAPLGP 12  
|||:|||||:  
Db 1834 QNVLLSNCPIDP 1845

RESULT 8  
D70914  
hypothetical protein Rv1425 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: D70914  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: D70914  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-459 <COL>  
A:Cross-references: GB:Z95844; GB:AL123456; NID:G3250713; PIDN:CAB09245.1; PID:e318877;  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: Rv1425

Query Match 52.5%; Score 41.5; DB 2; Length 459;  
Best Local Similarity 57.4%; Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 NIILSNAPLGP 15  
|:|:|:|:|:|:  
Db 380 NLVVSNP-GPPFP 392

RESULT 9  
AB2156  
hypothetical protein all2801 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AB2156  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AB2156  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-295 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA074500.1; PID:g17131894; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all2801

Query Match 51.9%; Score 41; DB 2; Length 295;  
Best Local Similarity 77.8%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 NAPLGPQFP 15  
|||||:  
Db 69 NAPLNPFP 77

RESULT 10  
AD1166  
probable peptidoglycan bound protein (LPXTG motif) lmo0732 [imported] - Listeria monocyt  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AD1166  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AD1166  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-638 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAC98810.1; PID:g16410121; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0732

Query Match 51.9%; Score 41; DB 2; Length 638;  
Best Local Similarity 58.3%; Pred. No. 45;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 NIILSNAPLGP 13  
|:|:|:|:|:|:  
Db 300 NVLIDNAPNPQP 311

RESULT 11  
D40228  
neurexin II-beta precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Dec-2002  
C:Accession: D40228; S27888  
R:Ushkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.  
Science 257, 50-56, 1992  
A:Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recep  
A:Reference number: A40228; MUID:92320296; PMID:1621094  
A:Accession: D40228



A/Status: preliminary; nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-662 <USH>  
A/Cross-references: GB:M96377; NID:g205717; PIDN:AAA41708.1; PID:g205719  
A/Note: authors translated GAC for residue 411 as Thr and ACC for residue 412 as Asp  
C/Superfamily: neurexin; EGF homology  
C/Keywords: alternative splicing; transmembrane protein  
F/1-47/Domain: signal sequence #status predicted <SIG>  
F/48-662/Product: neurexin II-beta #status predicted <MAT>  
Query Match 51.9%; Score 41; DB 2; Length 662;  
Best Local Similarity 66.7%; Pred. No. 47;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4 LLSNAPLGQFP 15  
DB 524 LLENPLPGVP 535  
RESULT 12  
S36337  
histidine decarboxylase (EC 4.1.1.22) - fruit fly (*Drosophila melanogaster*)  
C/Species: *Drosophila melanogaster*  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Jun-1999  
C/Accession: S36337  
R/Burg, M.G.; Sarthy, P.V.; Koliantz, G.; Pak, W.L.  
A/Title: Genetic and molecular identification of a *Drosophila* histidine decarboxylase gene  
A/Reference number: S36337; MUID:93209238; PMID:8096176  
A/Molecule type: mRNA  
A/Residues: 1-847 <BUR>  
A/Cross-references: EMBL:X70644; NID:g287837; PIDN:CAA49989.1; PID:g287838  
C/Genetics:  
A/Genes: FlyBase:Hdc  
A/Cross-references: FlyBase:FBgn0005619  
C/Superfamily: *Drosophila* histidine decarboxylase; animal histidine decarboxylase homolog  
C/Keywords: carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate  
F/2-470/Domain: animal histidine decarboxylase homology <HDC>  
F/124/Binding site: Pyridoxal phosphate (Lys) (covalent) #status predicted  
Query Match 51.9%; Score 41; DB 1; Length 847;  
Best Local Similarity 58.3%; Pred. No. 62;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 2 NTLNAPLGQ 13  
DB 500 SLLNSPLSPX 511  
RESULT 13  
C40228  
neurexin II-alpha precursor - rat  
C/Species: *Rattus norvegicus* (Norway rat)  
C/Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Dec-2002  
C/Accession: C40228; S27886; S27887  
R/Ushkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.  
Science 257, 50-56, 1992  
A/Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin receptor  
A/Reference number: A40228; MUID:92320296; PMID:1621094  
A/Accession: C40228  
A/Status: preliminary; nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-1715 <USH>  
A/Cross-references: GB:M96376; NID:g205714; PIDN:AAA41707.1; PID:g205716  
A/Note: authors translated the codon GAC for residue 1464 as Thr and ACC for residue 1465 as Thr  
R/Ushkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.  
submitted to the EMBL Data Library, July 1992  
A/Description: Neurexins: Synaptic cell surface proteins related to the alpha-latrotoxin  
A/Reference number: S27884  
A/Accession: S27886  
A/Molecule type: mRNA  
A/Residues: 1-1666, 'CRK', 1670, 'PRECKLLPG', 1683-1685, 'GL', 1688, 'LDLA', 1694-1695, 'CCVCRCRRA

A/Cross-references: EMBL:M96376; NID:g205714; PIDN:AAA41706.1; PID:g205715  
C/Genetics:  
A/Introns: 1666/2  
C/Superfamily: neurexin; EGF homology  
C/Keywords: alternative splicing; transmembrane protein  
F/1-27/Domain: signal sequence #status predicted <SIG>  
F/28-1715/Product: neurexin II-alpha #status predicted <MAT>  
F/694-726/Domain: EGF homology <EGF>  
F/1103-1135/Domain: EGF homology <EGF1>

Query Match 51.9%; Score 41; DB 2; Length 1715;  
Best Local Similarity 66.7%; Pred. No. 14e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 LLSNAPLGQFP 15

DB 1577 LLENPLPGVP 1588

# RESULT 14

C54258  
transcription factor HNF-3 gamma - mouse  
N/Alternate names: hepatocyte nuclear factor 3 gamma  
C/Species: *Mus musculus* (house mouse)  
C/Date: 18-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 18-Jun-1999  
C/Accession: C54258; S37186  
R/Kaestner, K.H.; Hiemisch, H.; Luckow, B.; Schutz, G.  
Genomics 20, 377-385, 1994  
A/Title: The HNF-3 gene family of transcription factors in mice: gene structure, cDNA sequence and expression  
A/Reference number: A54258; MUID:94307723; PMID:8034310  
A/Accession: C54258  
A/Molecule type: mRNA  
A/Residues: 1-353 <KAE>  
A/Cross-references: EMBL:X74938; NID:g402192; PIDN:CAA52892.1; PID:g402193  
C/Genetics:  
A/Introns: 23/3  
C/Function:  
A/Note: embryonic expression is later than HNF-3 alpha and beta, and tissue distribution  
C/Superfamily: transcription factor HNF-3; fork head DNA-binding domain homology  
C/Keywords: DNA binding; transcription factor  
F/119-210/Domain: fork head DNA-binding domain homology <FHD>

Query Match 50.6%; Score 40; DB 1; Length 353;  
Best Local Similarity 87.5%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 APLGQFP 15

DB 72 APLGQFP 79

# RESULT 15

S35090  
transcription factor HNF-3 gamma - rat  
C/Species: *Rattus norvegicus* (Norway rat)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C/Accession: S35090; A39533  
R/Lai, E.; Prezioso, V.R.; Tao, W.; Chen, W.S.; Darnell, J.E.  
submitted to the EMBL Data Library, January 1993  
A/Description: Hepatocyte nuclear factor 3a belongs to a gene family in mammals that is  
A/Reference number: S35090  
A/Accession: S35090  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-354 <LAI>  
A/Cross-references: EMBL:L09648; NID:g204624; PIDN:AAA41339.1; PID:g204625  
R/Lai, E.; Prezioso, V.R.; Tao, W.; Chen, W.S.; Darnell, J.E.  
Genes Dev. 5, 416-427, 1991  
A/Title: Hepatocyte nuclear factor 3a belongs to a gene family in mammals that is  
A/Reference number: A39533; MUID:91160974; PMID:1672118  
A/Accession: A39533  
A/Status: preliminary

A:Molecule type: mRNA  
 A:Residues: 'M',23,'GOEDRTT',31,'RQEDRAYVLF',43-44,'T',57-115,'A',117-354 <LA2>  
 A:Cross-references: GB:L09647  
 C:Superfamily: transcription factor HNF-3; fork head DNA-binding domain homology  
 C:Keywords: DNA binding; nucleus; transcription regulation  
 F:119-210/Domain: fork head DNA-binding domain homology <FHD>

Query Match 50.6%; Score 40; DB 1; Length 354;  
 Best Local Similarity 87.5%; Pred. No. 34;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 APLGQFP 15  
 |||||  
 Db 72 APLGTFP 79

Search completed: June 3, 2004, 15:15:25  
 Job time : 14.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:24 ; Search time 10 Seconds  
(without alignments)  
78.105 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70  
Perfect score: 79  
Sequence: 1 QNILLSNAPLGPQFP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	529	1 TYRO HUMAN	P14679 homo sapien
2	67	84.8	273	1 TYRO CANFA	P54834 canis famil
3	67	84.8	273	1 TYRO COTJA	Q08410 coturnix co
4	67	84.8	273	1 TYRO TRISI	P55026 trionyx sin
5	67	84.8	529	1 TYRO CHICK	P55024 gallus gall
6	63	79.7	533	1 TYRO MOUSE	P11344 mus musculu
7	49	62.0	532	1 TYRO RANNI	Q04604 rana nigrom
8	47	59.5	2131	1 YCF2 SPIOL	P08973 spinacia ol
9	47	59.5	2216	1 YCF2 EPIVI	P30072 epifagus vl
10	47	59.5	2280	1 YCF2 TOBAC	P09976 nicotiana t
11	45	57.0	2294	1 YCF2 ARATH	P56786 arabidopsis
12	44	55.7	426	1 TIG CHLTE	Q8kb57 chlorobium
13	41.5	52.5	459	1 YE43 MYCTU	P71694 mycobacteri
14	41	51.9	662	1 NX2B RAT	Q63376 rattus norv
15	41	51.9	847	1 DCHS DROME	Q05733 drosophila
16	41	51.9	1715	1 NX2A RAT	Q63374 rattus norv
17	41	51.9	2067	1 NCO6 MOUSE	Q9j119 m nuclear r
18	40	50.6	350	1 HN3G HUMAN	P55318 homo sapien
19	40	50.6	353	1 HN3G MOUSE	P35584 mus musculu
20	40	50.6	354	1 HN3G RAT	P32183 rattus norv
21	40	50.6	375	1 ACTG PENCH	Q9ur80 penicillium
22	40	50.6	666	1 NX2B HUMAN	P58401 homo sapien
23	40	50.6	1712	1 NX2A HUMAN	Q9p2a2 homo sapien
24	39	49.4	376	1 ACT1 TRYBB	P12432 trypanosoma
25	39	49.4	376	1 ACT2 TRYBB	P12433 trypanosoma
26	39	49.4	376	1 ACT TRYBB	P45520 leishmania
27	39	49.4	540	1 TYRO ORYLA	P55025 oryzias lat
28	39	49.4	1014	1 NANH CLOSE	P29767 clostridium
29	39	49.4	2298	1 YCF2 LOTJA	Q9b1k6 lotus japon
30	38.5	48.7	322	1 YD67 MYCPN	P75414 mycoplasma
31	38.5	48.7	502	1 YH60 MYCTU	Q06795 mycobacteri
32	38.5	48.7	669	1 HFO DROME	Q8t086 drosophila
33	38.5	48.7	1218	1 MGPC MYCPN	Q50341 mycoplasma

## RESULT 1

ID	TYRO HUMAN	STANDARD;	PRT;	529 AA.
AC	P14679; Q15675; Q15676; Q15680; Q8TAK4; Q9BYV0; Q9BZX1;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)			
DE	(Tumor rejection antigen AB) (SK29-AB) (LB24-AB).			
GN	TYR.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RX	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=91236163; PubMed=1903356;			
RA	Giebel L.B., Strunk K.M., Spritz R.A.;			
RT	"Organization and nucleotide sequences of the human tyrosinase gene			
RT	and a truncated tyrosinase-related segment.";			
RL	Genomics 9:435-445(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=88041128; PubMed=2823263;			
RA	Kwon B.S., Haq A.K., Pomerantz S.H., Halaban R.;			
RT	"Isolation and sequence of a cDNA clone for human tyrosinase that			
RT	maps at the mouse c-albino locus.";			
RN	[3]			
RN	Proc. Natl. Acad. Sci. U.S.A. 84:7473-7477(1987).			
RP	REVISIONS TO 384-398.			
RA	Kwon B.S., Haq A.K., Pomerantz S.H., Halaban R.;			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:6352-6352(1988).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Melanoma;			
RX	MEDLINE=89279151; PubMed=2493655;			
RA	Bouchard B., Fuller B.B., Vijayasaradhi S., Houghton A.N.;			
RT	"Induction of pigmentation in mouse fibroblasts by expression of			
RT	human tyrosinase cDNA.";			
RL	J. Exp. Med. 169:2029-2042(1989).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=91271371; PubMed=1711223;			
RA	Chintamaneni C.D., Halaban R., Kobayashi Y., Witkop C.J., Kwon B.S.;			
RT	"A single base insertion in the putative transmembrane domain of the			
RT	tyrosinase gene as a cause for tyrosinase-negative oculocutaneous			
RT	albinism.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5272-5276(1991).			
RN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Melanoma, and T-cell;			
RX	MEDLINE=93340625; PubMed=8340755;			
RA	Brichard V., van Pel A., Woelfel T., Woelfel C., de Plaen E.,			
RA	Lethe B., Coulie P., Boon T.;			
RT	"The tyrosinase gene codes for an antigen recognized by autologous			
RT	cytolytic T lymphocytes on HLA-A2 melanomas.";			

Q8y634 listeria mo  
Q92ae2 listeria in  
P02581 glycine max  
Q9w73 staphylococ  
Q8nxy7 staphylococ  
P30823 rattus norv  
Q9nrj7 homo sapien  
O70361 mus musculu  
P11799 gallus gall  
O27263 methanobact  
Q99x89 staphylococ  
Q9pp92 campylobact

## ALIGNMENTS

RL J. Exp. Med. 178:489-495(1993).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT TYR-192.  
RX MEDLINE=21026558; PubMed=11153699;  
RA Martinez-Arias R., Comas D., Andres A., Abello M.T., Domingo-Roura X.,  
RA Bertranpetit J.;  
RT "The tyrosinase gene in gorillas and the albinism of 'Snowflake'";  
RL Pigment Cell Res. 13:467-470(2000).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE OF 1-272 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=90089403; PubMed=2480811;  
RA Kikuchi H., Miura H., Yamamoto H., Takeuchi T., Dei T., Watanabe M.;  
RT "Characteristic sequences in the upstream region of the human  
RT tyrosinase gene";  
RL Biochim. Biophys. Acta 1009:283-286(1989).  
RN [10]  
RP SEQUENCE OF 1-32 FROM N.A.  
RX MEDLINE=89351001; PubMed=2504160;  
RA Takeda A., Tomita Y., Okinaga S., Tagami H., Shibahara S.;  
RT "Functional analysis of the cDNA encoding human tyrosinase  
RT precursor";  
RL Biochem. Biophys. Res. Commun. 162:984-990(1989).  
RN [11]  
RP SEQUENCE OF 54-195 FROM N.A., AND VARIANT TYR-192.  
RX MEDLINE=21082082; PubMed=11214319;  
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RA O'Brien S.J.;  
RT "Molecular phylogenetics and the origins of placental mammals";  
RL Nature 409:614-618(2001).  
RN [12]  
RP REVIEW ON OCA VARIANTS.  
RX MEDLINE=93237884; PubMed=8477259;  
RA Oetting W.S., King R.A.;  
RT "Molecular basis of type I (tyrosinase-related) oculocutaneous  
RT albinism: mutations and polymorphisms of the human tyrosinase gene";  
RL Hum. Mutat. 2:1-6(1993).  
RN [13]  
RP REVIEW ON OCA-I VARIANTS.  
RX MEDLINE=99140254; PubMed=10094567;  
RA Oetting W.S., King R.A.;  
RT "Molecular basis of albinism: mutations and polymorphisms of  
RT pigmentation genes associated with albinism";  
RL Hum. Mutat. 13:99-115(1999).  
RN [14]  
RP VARIANTS TYR-192; GLN-402; OCA-IA LYS-373 AND OCA-IA ASN-383.  
RX MEDLINE=90259036; PubMed=2342539;  
RA Spritz R.A., Strunk K.M., Giebel L.B., King R.A.;  
RT "Detection of mutations in the tyrosinase gene in a patient with type  
RT IA oculocutaneous albinism";  
RN New Engl. J. Med. 322:1724-1728(1990).  
RL [15]  
RP VARIANT OCA-IA LEU-81.  
RX MEDLINE=90238992; PubMed=1970634;  
RA Giebel L.B., Strunk K.M., King R.A., Hanifin J.M., Spritz R.A.;  
RT "A frequent tyrosinase gene mutation in classic, tyrosinase-negative  
RT (type IA) oculocutaneous albinism";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:3255-3258(1990).  
RN [16]  
RP VARIANTS OCA-IB PHE-275 AND LEU-406.  
RX MEDLINE=91241133; PubMed=1903591;  
RA Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,  
RA King R.A., Spritz R.A.;  
RT "Tyrosinase gene mutations associated with type IB ('yellow')  
RT oculocutaneous albinism";  
RL Am. J. Hum. Genet. 48:1159-1167(1991).  
RN [17]  
RP ERRATUM.  
RA Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,  
RA King R.A., Spritz R.A.;  
RL Am. J. Hum. Genet. 49:696-696(1991).  
RN [18]  
RP VARIANTS OCA-IA SER-21; TRP-217; HIS-299; SER-403; SER-446 AND  
RP ASN-448.  
RX MEDLINE=92351982; PubMed=1642278;  
RA Tripathi R.K., Strunk K.M., Giebel L.B., Weleber R.G., Spritz R.A.;  
RT "Tyrosinase gene mutations in type I (tyrosinase-deficient)  
RT oculocutaneous albinism define two clusters of missense  
RT substitutions";  
RL Am. J. Med. Genet. 43:865-871(1992).  
RN [19]  
RP VARIANT OCA-IA ARG-89.  
RX MEDLINE=91118940; PubMed=1899321;  
RA Spritz R.A., Strunk K.M., Hsieh C.-L., Sekhon G.S., Francke U.;  
RT "Homozygous tyrosinase gene mutation in an American black with  
RT tyrosinase-negative (type IA) oculocutaneous albinism";  
RL Am. J. Hum. Genet. 48:318-324(1991).  
RN [20]  
RP VARIANT OCA-ITS GLN-422.  
RX MEDLINE=91154384; PubMed=1900309;  
RA Giebel L.B., Tripathi R.K., King R.A., Spritz R.A.;  
RT "A tyrosinase gene missense mutation in temperature-sensitive type I  
RT oculocutaneous albinism. A human homologue to the Siamese cat and the  
RT Himalayan mouse";  
RL J. Clin. Invest. 87:1119-1122(1991).  
RN [21]  
RP VARIANTS OCA-IA GLY-42; TYR-55; THR-206 AND ARG-419.  
RX MEDLINE=92048465; PubMed=1943586;  
RA King R.A., Mentink M.M., Oetting W.S.;  
RT "Non-random distribution of missense mutations within the human  
RT tyrosinase gene in type I (tyrosinase-related) oculocutaneous  
RT albinism";  
RL Mol. Biol. Med. 8:19-29(1991).  
RN [22]  
RP VARIANTS OCA-IA ILE-176 AND GLN-217.  
RX MEDLINE=93138611; PubMed=1487241;  
RA Oetting W.S., King R.A.;  
RT "Molecular analysis of type I-A (tyrosinase negative) oculocutaneous  
RT albinism";  
RL Hum. Genet. 90:258-262(1992).  
RN [23]  
RP VARIANTS OCA-IA GLN-328; ARG-419 AND LEU-431.  
RX MEDLINE=94070862; PubMed=7902671;  
RA Tripathi R.K., Bunde S., Musarella M.A., Doretto S., Strunk K.M.,  
RA Holmes S.A., Spritz R.A.;  
RT "Mutations of the tyrosinase gene in Indo-Pakistani patients with type  
RT I (tyrosinase-deficient) oculocutaneous albinism (OCA)";  
RL Am. J. Hum. Genet. 53:1173-1179(1993).  
RN [24]  
RP VARIANTS OCA-IA ASP-47; CYS-217 DEL; HIS-299 AND LYS-373, AND VARIANTS  
RP OCA-IB SER-152 AND LYS-294.  
RX MEDLINE=94175072; PubMed=8128955;

Query Match 100.0%; Score 79; DB 1; Length 529;  
Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
DB 56 QNILLSNAPLGQPP 70

## RESULT 2

TYRO\_CANFA  
ID TYRO\_CANFA STANDARD; PRT; 273 AA.  
AC P54834;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)  
DE (Fragment).  
GN TYR.

OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Tang Q., Williams R.W., Hogan D., Valentine V., Goldowitz D.;  
RL Submitted (FEB-1996) to the EMBL/GenBank/DBP databases.

CC -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN  
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC  
COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO  
DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO  
INDOLE-5,6 QUINONE.

CC -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +  
DOPAquinone + H(2)O.

CC -!- COFACTOR: Binds 2 copper ions per subunit.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.

CC -!- SIMILARITY: Belongs to the tyrosinase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; U42219; AAA86420.1; -  
CC InterPro; IPR008922; Di-copper\_centre.

CC InterPro; IPR002227; Tyrosinase.

CC Pfam; PF00264; tyrosinase; 1.

CC PRINTS; PR00092; TYROSINASE.

CC PROSITE; PS00497; TYROSINASE 1; PARTIAL.

CC PROSITE; PS00498; TYROSINASE 2; PARTIAL.

KW Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;

KW Melanin biosynthesis.

FT SIGNAL 1 18

FT CHAIN 19 >273 POTENTIAL.

FT METAL 180 180 TYROSINASE.

FT METAL 202 202 COPPER A (BY SIMILARITY).

FT METAL 211 211 COPPER A (BY SIMILARITY).

FT CARBOHYD 86 86 COPPER A (BY SIMILARITY).

FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT NON TER 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 273 AA; 31081 MW; A65725E69B2E9792 CRC64;

Query Match 84.8%; Score 67; DB 1; Length 273;  
Best Local Similarity 80.0%; Pred. No. 0.00027;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15

DB 56 QDIVLSNAPFGQPP 70

## RESULT 3

TYRO\_COTJA  
ID TYRO\_COTJA STANDARD; PRT; 273 AA.  
AC Q08410;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)  
DE (Fragment).  
GN TYR.

OS Coturnix coturnix japonica (Japanese quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Coturnix.

OX NCBI\_TaxID=93934;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=93181407; PubMed=1292011;

RA Yamamoto H., Kudo T., Masuko N., Miura H., Sato S., Tanaka M.,

RA Tanaka S., Takeuchi S., Shibahara S., Takeuchi T.;

RT "Phylogeny of regulatory regions of vertebrate tyrosinase genes.";

RL Pigment Cell Res. 5:284-294(1992).

CC -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN  
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC  
COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO  
DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO  
INDOLE-5,6 QUINONE.

CC -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +  
DOPAquinone + H(2)O.

CC -!- COFACTOR: Binds 2 copper ions per subunit.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.

CC -!- SIMILARITY: Belongs to the tyrosinase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; S56788; AAB25510.1; -

CC InterPro; IPR008922; Di-copper\_centre.

CC InterPro; IPR002227; Tyrosinase.

CC Pfam; PF00264; tyrosinase; 1.

CC PRINTS; PR00092; TYROSINASE.

CC PROSITE; PS00497; TYROSINASE 1; 1.

CC PROSITE; PS00498; TYROSINASE 2; PARTIAL.

KW Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;

KW Transmembrane; Melanin biosynthesis.

FT SIGNAL 1 18

FT CHAIN 19 >273 POTENTIAL.

FT METAL 180 180 TYROSINASE.

FT METAL 202 202 COPPER A (BY SIMILARITY).

FT METAL 211 211 COPPER A (BY SIMILARITY).

FT CARBOHYD 86 86 COPPER A (BY SIMILARITY).

FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT NON TER 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 273 AA; 31499 MW; 0EA3DE55BE11E1A1A CRC64;

Query Match 84.8%; Score 67; DB 1; Length 273;  
Best Local Similarity 86.7%; Pred. No. 0.00027;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15

DB 56 QRILLSQAPLGQPP 70

```

RESULT 4
TYRO_TRISI
ID TYRO_TRISI STANDARD; PRT; 273 AA.
AC P55026;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
DE (Fragment)
GN TYR.

OS Trionyx sinensis (Chinese softshell turtle) (Pelodiscus sinensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Trionychoidea; Trionychidae; Pelodiscus.
OX NCBI_TaxID=13735;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ssp. Japonicus; TISSUE=Testis;
RX MEDLINE=93181407; PubMed=1292011;
RA Yamamoto H., Kudo T., Masuko N., Miura H., Sato S., Tanaka M.,
RA Tanaka S., Takeuchi S., Shibahara S., Takeuchi T.;
RT "Phylogeny of regulatory regions of vertebrate tyrosinase genes.";
RL Pigment Cell Res. 5:284-294(1992).
CC -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
CC THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
CC COMPOUNDS.
CC -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
CC DOPAQUINONE + H(2)O.
CC -!- COFACTOR: Binds 2 copper ions per subunit.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
CC -!- SIMILARITY: Belongs to the tyrosinase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S56789; AAB25511.1; -.
CC InterPro; IPR008922; Di-copper_centre.
CC InterPro; IPR002227; Tyrosinase.
CC Pfam; PF00264; Tyrosinase; 1.
CC PRINTS; PR00092; TYROSINASE.
CC PROSITE; PS00497; TYROSINASE_1; 1.
CC PROSITE; PS00498; TYROSINASE_2; PARTIAL.
CC Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
CC Transmembrane; Melanin biosynthesis.
CC SIGNAL 1 18 POTENTIAL.
CC CHAIN 1 19 273 TYROSINASE.
CC METAL 180 180 COPPER A (BY SIMILARITY).
CC METAL 202 202 COPPER A (BY SIMILARITY).
CC METAL 211 211 COPPER A (BY SIMILARITY).
CC CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
CC NON TER 273 273
CC SEQUENCE 273 AA; 31136 MW; 9365C76EDB26A625 CRC64;

Query Match 84.8%; Score 67; DB 1; Length 273;
Best Local Similarity 86.7%; Pred. No. 0.00027;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ONILLSNAPLGQFP 15
Db 56 QEILSRAPLGQFP 70

RESULT 5
TYRO_CHICK
ID TYRO_CHICK STANDARD; PRT; 529 AA.
AC P55024;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
DE TYR.
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn;
RX MEDLINE=93157254; PubMed=1494538;
RA Mochii M., Iio A., Yamamoto H., Takeuchi T., Eguchi G.;
RT "Isolation and characterization of a chicken tyrosinase cDNA.";
RL Pigment Cell Res. 5:162-167(1992).
CC [2]
CC SEQUENCE OF 1-273 FROM N.A.
CC MEDLINE=96194800; PubMed=8647445;
CC Ferguson C.A., Kidson S.H.;
CC "Characteristic sequences in the promoter region of the chicken
CC tyrosinase-encoding gene.";
CC Gene 169:191-195(1996).
CC -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
CC THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
CC COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO
CC DOPA. DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO
CC INDOLE-5,6 QUINONE.
CC -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
CC DOPAQUINONE + H(2)O.
CC -!- COFACTOR: Binds 2 copper ions per subunit.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
CC -!- SIMILARITY: Belongs to the tyrosinase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D80349; BAA13590.1; -.
CC EMBL; L46805; AAB08441.1; -.
CC PIR; PC4153; PC4153.
CC InterPro; IPR008922; Di-copper_centre.
CC InterPro; IPR002227; Tyrosinase.
CC Pfam; PF00264; Tyrosinase; 1.
CC PRINTS; PR00092; TYROSINASE.
CC PROSITE; PS00497; TYROSINASE_1; 1.
CC PROSITE; PS00498; TYROSINASE_2; 1.
CC Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
CC Transmembrane; Melanin biosynthesis.
CC SIGNAL 1 18 POTENTIAL.
CC CHAIN 1 19 529 TYROSINASE.
CC DOMAIN 19 476 LUMENAL, MELANOSOME (POTENTIAL).
CC TRANSMEM 477 497 POTENTIAL.
CC DOMAIN 498 529 CYTOPLASMIC (POTENTIAL).
CC METAL 180 180 COPPER A (BY SIMILARITY).
CC METAL 202 202 COPPER A (BY SIMILARITY).
CC METAL 211 211 COPPER A (BY SIMILARITY).
CC METAL 363 363 COPPER B (BY SIMILARITY).
CC METAL 367 367 COPPER B (BY SIMILARITY).
CC METAL 390 390 COPPER B (BY SIMILARITY).
CC CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 111 111 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 337 337 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).

```

FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 529 AA; 60357 MW; 74B464A52C3FFBFS CRC64;  
 Query Match 84.8%; Score 67; DB 1; Length 529;  
 Best Local Similarity 86.7%; Pred. No. 0.00057;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 QNILLSNAPLGPQFP 15  
 Db 56 QRILLSQAPLGPQFP 70

RESULT 6  
 ID TYRO MOUSE STANDARD; PRT; 533 AA.  
 AC P11344;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tyrosinase precursor (RC 1.14.18.1) (Monophenol monooxygenase)  
 DE (Albino locus protein).  
 GN TYR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DRB/2J;  
 RX MEDLINE=89268910; PubMed=3134020;  
 RA Kwon B.S., Makulchik M., Haq A.K., Halaban R., Kestler D.;  
 RT "Sequence analysis of mouse tyrosinase cDNA and the effect of  
 RT melanotropin on its gene expression."  
 RL Biochem. Biophys. Res. Commun. 153:1301-1309(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Himalayan;  
 RX MEDLINE=89273644; PubMed=2567165;  
 RA Kwon B.S., Halaban R., Chintamaneni C.;  
 RT "Molecular basis of mouse Himalayan mutation."  
 RL Biochem. Biophys. Res. Commun. 161:252-260(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89030636; PubMed=3141148;  
 RA Mueller G., Ruppert S., Schmid E., Schuetz G.;  
 RT "Functional analysis of alternatively spliced tyrosinase gene  
 RT transcripts."  
 RL EMBO J. 7:2723-2730(1988).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89193679; PubMed=2494997;  
 RA Terao M., Tabe L., Garattini E., Sartori D., Studer M., Mintz B.;  
 RT "Isolation and characterization of variant cDNAs encoding mouse  
 RT tyrosinase."  
 RL Biochem. Biophys. Res. Commun. 159:848-853(1989).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J;  
 RA Yamamoto H., Takeuchi S., Kudo T., Makino K., Nakata A., Shinoda T.,  
 RA Takeuchi T.;  
 RT "Cloning and sequencing of mouse tyrosinase cDNA."  
 RL Jpn. J. Genet. 62:271-274(1987).  
 RN [6]  
 RP SEQUENCE OF 1-273 FROM N.A.  
 RX MEDLINE=90212084; PubMed=2517217;  
 RA Yamamoto H., Takeuchi S., Kudo T., Sato C., Takeuchi T.;  
 RT "Melanin production in cultured albino melanocytes transfected with  
 RT mouse tyrosinase cDNA."  
 RL Jpn. J. Genet. 64:121-135(1989).  
 RN [7]  
 RP VARIANT ALBINO.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=90249393; PubMed=2110899;

RA Shibahara S., Okinaga S., Tomita Y., Takeda A., Yamamoto H., Sato M.,  
 RA Takeuchi T.;  
 RT "A point mutation in the tyrosinase gene of BALB/c albino mouse  
 RT causing the cysteine-->serine substitution at position 85."  
 RL Eur. J. Biochem. 189:455-461(1990).  
 RN [8]  
 RP VARIANT CHINCHILLA MICE.  
 RX MEDLINE=90360993; PubMed=2118105;  
 RA Beermann F., Ruppert S., Hummler E., Bosch F.X., Mueller G.,  
 RA Ruether U., Schuetz G.;  
 RT "Rescue of the albino phenotype by introduction of a functional  
 RT tyrosinase gene into mice."  
 RL EMBO J. 9:2819-2826(1990).  
 CC -1- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN  
 CC THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC  
 CC COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO  
 CC DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO  
 CC INDOLE-5,6 QUINONE.  
 CC -1- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +  
 CC DOPAquinone + H(2)O.  
 CC -1- COFACTOR: Binds 2 copper ions per subunit.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.  
 CC -1- DISEASE: DEFECTS IN TYR RESULT IN VARIOUS FORMS OF ALBINISM.  
 CC HIMALAYAN STRAIN TYROSINASE IS TEMPERATURE-SENSITIVE.  
 CC -1- SIMILARITY: Belongs to the tyrosinase family.  
 CC -1- CAUTION: REF.4 SEQUENCE WAS INCORRECT DUE TO A DELETION OF EXON 3.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; D00440; BAA00341.1; -;  
 DR EMBL; M20234; AAA00516.1; -;  
 DR EMBL; M26729; AAA37806.1; -;  
 DR EMBL; X12782; CAA31273.1; -;  
 DR EMBL; M24560; AAA40517.1; -;  
 DR EMBL; D00131; BAA00079.1; -;  
 DR EMBL; X51743; CAA36033.1; -;  
 DR EMBL; D00439; BAA00340.1; -;  
 DR PIR; A27711; YRMSCS.  
 DR MGD; MG1:98880; Tyr.  
 DR InterPro; IPR008922; Di-copper centre.  
 DR InterPro; IPR002227; Tyrosinase.  
 DR Pfam; PF00284; tyrosinase; 1.  
 DR PRINTS; PR00092; TYROSINASE.  
 DR PROSITE; PS00497; TYROSINASE 1; 1.  
 DR PROSITE; PS00498; TYROSINASE 2; 1.  
 DR Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;  
 KW Transmembrane; Melanin biosynthesis; Disease mutation; Albinism.  
 FT SIGNAL 1 18  
 FT CHAIN 19 533  
 FT DOMAIN 19 476  
 FT TRANSMEM 477 497  
 FT DOMAIN 498 533  
 FT METAL 180 180  
 FT METAL 202 202  
 FT METAL 211 211  
 FT METAL 363 363  
 FT METAL 367 367  
 FT METAL 390 390  
 FT DOMAIN 503 508  
 FT CARBOHYD 86 86  
 FT CARBOHYD 111 111  
 FT CARBOHYD 161 161  
 FT CARBOHYD 230 230  
 FT CARBOHYD 337 337  
 FT CARBOHYD 371 371  
 FT VARIANT 103 103  
 FT VARIANT 420 420  
 H -> R (IN HIMALAYAN STRAIN).

FT VARIANT 482 482 A -> T (IN CHINCHILLA MICE).  
 FT CONFLICT 40 40 M -> I (IN REF. 2).  
 FT CONFLICT 197 197 D -> Q (IN REF. 2).  
 FT CONFLICT 264 264 S -> I (IN REF. 3).  
 FT CONFLICT 346 346 V -> G (IN REF. 2, 3 AND 4).  
 FT CONFLICT 348 356 ASPGTGIAD -> LFEHNGCEG (IN REF. 5).  
 FT CONFLICT 357 403 MISSING (IN REF. 5).  
 FT CONFLICT 471 495 ASRWPLLGAALVGAIAAALSG -> GQSYLAMASWGS  
 FT CONFLICT 496 533 TGGSCYCCSSLWA (IN REF. 5).  
 FT CONFLICT 533 AA; 60648 MW; 4B711312DDBG6F7D1 CRC64;  
 SQ SEQUENCE 533 AA; 60648 MW; 4B711312DDBG6F7D1 CRC64;  
 Query Match 79.7%; Score 63; DB 1; Length 533;  
 Best Local Similarity 80.0%; Pred. No. 0.0029;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 QNILLSNAPLGQPP 15  
 Db 56 QDILLSSAPGQPP 70  
 RESULT 7  
 TYRO\_RANNI STANDARD; PRT; 532 AA.  
 ID TYRO\_RANNI STANDARD; PRT; 532 AA.  
 AC Q04604;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).  
 GN TYR OR TYRS.  
 OS Rana nigromaculata (Japanese pond frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8409;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93077054; PubMed=1446833;  
 RA Takase M., Miura I., Nakata A., Takeuchi T., Nishioka M.;  
 RT "Cloning and sequencing of the cDNA encoding tyrosinase of the  
 Japanese pond frog, Rana nigromaculata.";  
 RL Gene 121:359-363 (1992).  
 RN [2]  
 RP SEQUENCE OF 1-277 FROM N.A.  
 RC TISSUE=Blood;  
 RA Miura I., Okumoto H., Makino K., Nakata A., Nishioka M.;  
 RT "Analysis of the tyrosinase gene of the Japanese pond frog, Rana  
 nigromaculata: cloning and nucleotide sequence of the genomic DNA  
 containing the tyrosinase gene and its flanking regions.";  
 RL Jpn. J. Genet. 70:79-82 (1995).  
 CC -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN  
 CC THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC  
 CC COMPOUNDS.  
 CC -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +  
 CC DOPAquinone + H(2)O.  
 CC -!- COFACTOR: Binds 2 copper ions per subunit.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.  
 CC -!- SIMILARITY: Belongs to the tyrosinase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: D12514; BAA02077.1; -;  
 CC EMBL: D37779; BAA07034.1; -;  
 CC PIR: JCI1392; JCI1392;  
 CC InterPro: IPR008922; Di-copper\_centre.  
 CC InterPro: IPR002227; Tyrosinase.  
 CC Pfam: PF00264; tyrosinase; 1.

DR PRINTS: PR00092; TYROSINASE.  
 DR PROSITE; PS00497; TYROSINASE\_1; 1.  
 DR PROSITE; PS00498; TYROSINASE\_2; 1.  
 KW Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;  
 KW Transmembrane; Melanin biosynthesis.  
 FT SIGNAL 1 19  
 FT CHAIN 20 532  
 FT DOMAIN 20 475  
 FT TRANSFEM 476 499  
 FT DOMAIN 500 532  
 FT METAL 184 184  
 FT METAL 206 206  
 FT METAL 215 215  
 FT METAL 367 367  
 FT METAL 371 371  
 FT METAL 394 394  
 FT CARBOHYD 90 90  
 FT CARBOHYD 115 115  
 FT CARBOHYD 165 165  
 FT CARBOHYD 234 234  
 FT CARBOHYD 341 341  
 FT CARBOHYD 375 375  
 FT VARIANT 10 10  
 SQ SEQUENCE 532 AA; 60115 MW; B27D3080F0C74B3A CRC64;  
 Query Match 62.0%; Score 49; DB 1; Length 532;  
 Best Local Similarity 53.3%; Pred. No. 0.8;  
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 QNILLSNAPLGQPP 15  
 Db 60 QDVVPSNPVGAQPP 74  
 RESULT 8  
 YCF2\_SPIOL STANDARD; PRT; 2131 AA.  
 ID YCF2\_SPIOL STANDARD; PRT; 2131 AA.  
 AC P08973; Q9M312;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 250 kDa protein ycf2 (ORF 2131).  
 GN YCF2.  
 OS Spinacia oleracea (Spinach).  
 CC Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
 CC Caryophyllales; Amaranthaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88295221; PubMed=2841033;  
 RA Zhou D.X., Massenet O., Quigley F., Marion M.J., Monseger F.,  
 RA Huber P., Mache R.;  
 RT "Characterization of a large inversion in the spinach chloroplast  
 genome relative to Marchantia: a possible transposon-mediated  
 origin.";  
 RL Curr. Genet. 13:433-439 (1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Geant d'hiver, and cv. Monatol;  
 RX MEDLINE=21187424; PubMed=11292076;  
 RA Schmitz-Linneweber C., Maier R.M., Alcaraz J.-P., Cottet A.,  
 RA Hermann R.G., Mache R.;  
 RT "The plastid chromosome of spinach (Spinacia oleracea): complete  
 nucleotide sequence and gene organization.";  
 RL Plant Mol. Biol. 45:307-315 (2001).  
 CC -!- SIMILARITY: Belongs to the ycf2 family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way



CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; X07908; CAA30743.1; -;  
 DR EMBL; AJ400848; CAB88802.1; -;  
 DR PIR; S01446; S01446.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003959; AAA\_ATPase\_cent.  
 DR InterPro; IPR008543; DUF825.  
 DR Pfam; PF00004; AAA; 1.  
 DR Pfam; PF05695; DUF825; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR Chloroplast; Hypothetical protein.  
 KW CONFLICT 853 I -> T (IN REF. 1).  
 FT CONFLICT 937 K -> N (IN REF. 1).  
 FT CONFLICT 973 T -> P (IN REF. 1).  
 FT CONFLICT 973 T -> T (IN REF. 1).  
 FT CONFLICT 1946 S -> T (IN REF. 1).  
 FT CONFLICT 1946 S -> T (IN REF. 1).  
 SQ SEQUENCE 2131 AA; 249980 MW; 915CCF87D1C32E31 CRC64;

Query Match 59.5%; Score 47; DB 1; Length 2131;  
 Best Local Similarity 66.7%; Pred. No. 8.5;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGP 12

Db 1742 QNVLLSNCPIDP 1753

RESULT 9

ID YCF2\_EPIVI STANDARD; PRT; 2216 AA.  
 AC P30072;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical 259.5 kDa protein Ycf2 (ORF 2216).  
 GN YCF2-A AND YCF2-B.  
 OS Epifagus virginiana (Beechdrops).  
 OG Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 CC lamids; Lamiales; Orobanchaceae; Orobanchaceae; Epifagus.  
 CC NCBI\_TaxID=4177;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93066301; PubMed=1332054;  
 RA Wolfe K.H., Morden C.W., Palmer J.D.;  
 RT "Function and evolution of a minimal plastid genome from a  
 RT nonphotosynthetic parasitic plant."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652 (1992).  
 CC -!- SIMILARITY: Belongs to the ycf2 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; M81884; AAA65867.1; -;  
 DR EMBL; M81884; AAA65873.1; -;  
 DR PIR; S78398; S78398.  
 DR InterPro; IPR003959; AAA\_ATPase\_cent.  
 DR InterPro; IPR008543; DUF825.  
 DR Pfam; PF00004; AAA; 1.  
 DR Pfam; PF05695; DUF825; 1.  
 KW Chloroplast; Hypothetical protein.  
 SQ SEQUENCE 2216 AA; 259511 MW; E2D9B5A4E9488DFF CRC64;

Query Match 59.5%; Score 47; DB 1; Length 2216;  
 Best Local Similarity 66.7%; Pred. No. 8.9;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 QNILLSNAPLGP 12  
 Db 1834 QNVLLSNCPIDP 1845

RESULT 10

ID YCF2\_TOBAC STANDARD; PRT; 2280 AA.  
 AC P09976; P09977;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 267 kDa protein ycf2 (ORF 2280).  
 GN YCF2.  
 OS Nicotiana tabacum (Common tobacco).  
 OG Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 CC lamids; Solanales; Solanaceae; Nicotiana.  
 CC NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Bright Yellow 4;  
 RA Shinzaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,  
 RA Matsubayashi T., Zaita N., Chunwongse J., Obokata J.,  
 RA Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.-Y., Sugita M.,  
 RA Deno H., Kanogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,  
 RA Tohdoh N., Shimada H., Sugiura M.;  
 RT "The complete nucleotide sequence of the tobacco chloroplast genome:  
 RT its gene organization and expression."  
 RL EMBL J. 5:2043-2049 (1986).  
 RN [2]

RP REVISIONS.

RA Sugiura M.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Not yet known.  
 CC -!- SIMILARITY: Belongs to the ycf2 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; Z00044; CAA77427.1; -;  
 DR EMBL; Z00044; CAA77438.1; -;  
 DR PIR; A05204; A05204.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003959; AAA\_ATPase\_cent.  
 DR InterPro; IPR008543; DUF825.  
 DR Pfam; PF00004; AAA; 1.  
 DR Pfam; PF05695; DUF825; 1.  
 DR SMART; SM00382; AAA; 1.  
 KW Chloroplast; Hypothetical protein.  
 SQ SEQUENCE 2280 AA; 266812 MW; E246D5F3D902C06D CRC64;

Query Match 59.5%; Score 47; DB 1; Length 2280;  
 Best Local Similarity 66.7%; Pred. No. 9.2;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGP 12

Db 1906 QNVLLSNCPIDP 1917

RESULT 11

ID YCF2\_ARATH  
 AC P56786;  
 STANDARD; PRT; 2294 AA.

30-MAY-2000 (Rel. 39, Created)  
30-MAY-2000 (Rel. 39, Last sequence update)  
30-MAY-2003 (Rel. 41, Last annotation update)  
Hypothetical 269.6 kDa protein ycf2  
(YCF2-A OR YCF2-1 OR ATCG00860) AND (YCF2-B OR YCF2-2 OR ATCG01280).  
Arabidopsis thaliana (Mouse-ear cross).  
Chloroplast.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
NCBI\_TaxID=3702;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=20039611; PubMed=10574454;  
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;  
RT "Complete structure of the chloroplast genome of Arabidopsis  
thaliana.";  
RL DNA Res. 6:283-290(1999).  
CC -!- SIMILARITY: Belongs to the ycf2 family.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; AP000423; BAA84428.1; -;  
EMBL; AP000423; BAA84449.1; -;  
DR InterPro; IPR003593; AAA ATPase.  
DR InterPro; IPR003959; AAA ATPase\_cent.  
DR InterPro; IPR008543; DUF825.  
DR Pfam; PF00004; AAA; 1.  
DR Pfam; PF05695; DUF825; 1.  
DR SMART; SMO0362; AAA; 1.  
DR Chloroplast; Hypothetical protein.  
SQ SEQUENCE 2294 AA; 269563 MW; 6A1BE7291DF30886 CRC64;  
-----  
Query Match 57.0%; Score 45; DB 1; Length 2294;  
Best Local Similarity 58.3%; Pred. No. 21;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
OY 1 QNVLISNAPLGP 12  
DB 1917 QNVLISNCPIDP 1928  
-----  
RESULT 12  
TIG CHLTP  
ID TIG CHLTP STANDARD; PRT; 426 AA.  
AC Q8KE57;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Trigger factor (TF).  
GN TIG OR CT1934.  
OS Chlorobium tepidum.  
OC Bacteria; Chlorobi; Chlorobiales; Chlorobiaceae;  
OC Chlorobium.  
OX NCBI\_TaxID=1097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 49652 / DSM 12025;  
RX MEDLINE=22103685; PubMed=12093901;  
RA Eison J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,  
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,  
RA Hickey B.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,  
RA Holt I., Unayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,  
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,  
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,  
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

RT "The complete genome sequence of Chlorobium tepidum TLS, a  
photosynthetic, anaerobic, green-sulfur bacterium.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).  
CC -!- FUNCTION: Involved in protein export. Acts as a chaperone by  
maintaining the newly synthesized protein in an open conformation  
(by similarity).  
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family. TIG subfamily.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; AE012944; AMW73153.1; -;  
TIG; CT1934;  
DR HAMAP; MF\_00303; -; 1.  
DR InterPro; IPR001179; FKBP\_PPIase.  
DR InterPro; IPR005215; Trig fac.  
DR InterPro; IPR008880; Trigger\_C.  
DR InterPro; IPR008881; Trigger\_N.  
DR Pfam; PF00254; FKBP; 1.  
DR Pfam; PF05698; Trigger\_C; 1.  
DR Pfam; PF05697; Trigger\_N; 1.  
DR TIGRfams; TIGR00115; tlg; 1.  
DR PROSITE; PS00453; FKBP\_PPIASE\_1; FALSE NEG.  
DR PROSITE; PS00454; FKBP\_PPIASE\_2; FALSE NEG.  
DR PROSITE; PS00059; FKBP\_PPIASE\_3; FALSE NEG.  
DR Cell division; Chaperone; Isomerase; Rotamase; Complete proteome.  
KW DOMAIN 160 240 PPIASE, FKBP-TYPE.  
FT SEQUENCE 426 AA; 48608 MW; AFC3C50F48C8C2F4 CRC64;  
SQ SEQUENCE 426 AA; 48608 MW; AFC3C50F48C8C2F4 CRC64;  
-----  
Query Match 55.7%; Score 44; DB 1; Length 426;  
Best Local Similarity 64.7%; Pred. No. 4.7;  
Matches 11; Conservative 1; Mismatches 3; Indels 2; Gaps 1;  
OY 1 QNILLSNA--PLGQFP 15  
DB 306 QNILLNAXRQVGQFP 322  
-----  
RESULT 13  
ID YE43 MYCTU STANDARD; PRT; 459 AA.  
AC P71694; O06833;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical protein RV1425/MT1468.  
GN RV1425 OR MT1468 OR MTCY21B4.43 OR MTCY493.29C.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RX MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala E.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,  
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Ruster S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sulston J.E., Taylor K., Whitthead S., Barrall B.G.;  
RT "Deciphering the biology of Mycobacterium tuberculosis from the  
complete genome sequence.";  
RL Nature 393:537-544(1998).  
RN [2]  
RP SEQUENCE FROM N.A.



FT DOMAIN 318 321 POLY-THR.  
FT DOMAIN 324 327 POLY-THR.  
FT DOMAIN 394 397 POLY-PRO.  
FT DOMAIN 594 597 POLY-ALA.  
FT VARSPLIC 203 232 Missing (in isoform 3, isoform 4, isoform 7 and isoform 8).  
FT VARSPLIC /FTid=VSP\_003518.  
FT VARSPLIC 368 385 Missing (in isoform 2, isoform 4, isoform 6 and isoform 8).  
FT VARSPLIC /FTid=VSP\_003519.  
FT VARSPLIC 614 662 DEGSYQVDSNSVYISNSAQSNGAVVKEKAPAKPTPSKAKK  
FT VARSPLIC NCNEYIV -> CRKSPEEKLLGSAQGLDLAKACVC  
FT VARSPLIC RCRATCIAGKPLERGGRGGERQMIIYIKNK (in isoform 5, isoform 6, isoform 7 and isoform 8).  
FT VARSPLIC /FTid=VSP\_003520.  
SQ SEQUENCE 662 AA; 70546 MW; A362EFFI85F2B56B CRC64;

Query Match 51.9%; Score 41; DB 1; Length 662;  
Best Local Similarity 66.7%; Pred. No. 26;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 LLSNAPLGQPP 15  
Db 524 LLENPLGPGVP 535

RESULT 15  
DCHS DROME STANDARD; PRT; 847 AA.  
AC Q05733;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Histidine decarboxylase (EC 4.1.1.22) (HDC).  
GN HDC.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93209238; PubMed=8096176;  
RA Burg M.G., Sarthy P.V., Koliantz G., Pak W.I.;  
RT "Genetic and molecular identification of a Drosophila histidine decarboxylase gene required in photoreceptor transmitter synthesis.";  
RL EMBL J. 12:911-919(1993).  
CC -!- FUNCTION: Required in photoreceptor transmitter synthesis.  
CC -!- CATALYTIC ACTIVITY: L-histidine = histamine + CO(2).  
CC -!- COFACTOR: Pyridoxal phosphate.  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SIMILARITY: Belongs to the group II decarboxylase family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL; X70644; CAA49989.1; -.  
CC PIR; S36337; S36337.  
CC FlyBase; FBgn0005619; Hdc.  
CC InterPro; IPR002129; Pyridoxal dec.  
CC Pfam; PF00282; Pyridoxal\_dec; 1.  
CC PRINTS; PR00800; YHDCRBOXLASE.  
CC PROSITE; PS00392; DDC GAD HDC YDC; 1.  
CC Lysase; Decarboxylase; Catecholamine biosynthesis; Pyridoxal phosphate.  
FT BINDING 304 304 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
SQ SEQUENCE 847 AA; 94106 MW; 6DFDE7B9034BC8F CRC64;

Query Match 51.9%; Score 41; DB 1; Length 847;  
Best Local Similarity 58.3%; Pred. No. 34;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 2 NILSNAPLGQP 13  
Db 500 SLLSNSPLSPK 511  
Search completed: June 3, 2004, 15:14:45  
Job time : 11 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:24 ; Search time 36.5 Seconds  
(without alignments)  
129.665 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70

Perfect score: 79

Sequence: 1 QNILLSNAPLGQFP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREML\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Description
1	79	100.0	Q9BEP2 ateles fusc
2	79	100.0	Q9BEP0 hylobates c
3	79	100.0	Q9BEP1 macaca mula
4	79	100.0	Q9GLU6 gorilla gor
5	79	100.0	Q9GLU8 pygathrix n
6	79	100.0	Q9GLT6 pygathrix a
7	79	100.0	Q9GLV0 pan troglod
8	79	100.0	Q9GLV2 papio hamad
9	79	100.0	Q9GLS4 pygathrix r
10	79	100.0	Q9GLS6 macaca thib
11	79	100.0	Q9GLS0 trachypithe
12	79	100.0	Q9GLS6 trachypithe
13	79	100.0	Q9GLS2 trachypithe
14	79	100.0	Q9GLV4 macaca neme
15	79	100.0	Q9GLT4 nasalis lar
16	79	100.0	Q9GLR8 pygathrix b

17	79	100.0	388	6	Q9GKN0
18	79	100.0	388	6	Q9GLT0
19	79	100.0	388	6	Q9GLU4
20	79	100.0	388	6	Q9GKM8
21	79	100.0	388	6	Q9GLU2
22	79	100.0	388	6	Q9GLT8
23	79	100.0	388	6	Q9GLT2
24	79	100.0	388	6	Q9GLU0
25	79	100.0	388	6	Q9GLU8
26	79	100.0	529	6	Q9BDE0
27	78	98.7	142	6	Q9BEP6
28	76	96.2	142	6	Q9BEN6
29	76	96.2	142	6	Q9BEN7
30	75	94.9	142	11	Q9BNK8
31	74	93.7	142	6	Q9BEP5
32	74	93.7	142	6	Q9BEQ3
33	74	93.7	142	11	Q9BNK9
34	73	92.4	142	6	Q9BEQ2
35	73	92.4	142	6	Q9BEP7
36	73	92.4	142	6	Q9BEQ1
37	73	92.4	142	11	Q9BNL0
38	73	92.4	530	6	Q9MYI7
39	72	91.1	142	6	Q9BEN9
40	71	89.9	142	6	Q9BEM5
41	71	89.9	142	6	Q9BEP8
42	70	88.6	142	6	Q8MK74
43	70	88.6	142	6	Q9BEQ7
44	70	88.6	142	11	Q9BNK3
45	70	88.6	142	11	Q9BNK4

#### ALIGNMENTS

#### RESULT 1

Q9BEP2 ID Q9BEP2 PRELIMINARY; PRT; 142 AA.  
AC Q9BEP2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Tyrosinase (Fragment).  
GN TYR.  
OS Ateles fusciceps (Brown-headed spider monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.  
OX NCBI\_TaxID=9508;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082082; PubMed=11214319;  
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RA O'Brien S.J.;  
RT "Molecular phylogenetics and the origins of placental mammals.";  
RL Nature 409:614-618(2001).  
DR EMBL; AY012015; AAG38758.1; -.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0005198; P:structural molecule activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR008922; Di-copper\_centre.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR002227; Tyrosinase.  
DR Pfam; PF0264; tyrosinase; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1.  
FT NON\_TER 1  
FT NON\_TER 142  
SQ SEQUENCE 142 AA; 16198 MW; 50100B8C49A371D5 CRC64;

Query Match 100.0%; Score 79; DB 6; Length 142;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 QNILLSNAPLGPOFP 15
Db 3 QNILLSNAPLGPOFP 17

RESULT 2
ID Q9BEP0 PRELIMINARY; PRT; 142 AA.
AC Q9BEP0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (Fragment).
GN TYR.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=23089;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY012017; AAG38760.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
FT NON_TER 142
FT NON_TER 142
SQ SEQUENCE 142 AA; 16230 MW; 4CCCA44BA849D227 CRC64;

Query Match 100.0%; Score 79; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPOFP 15
Db 3 QNILLSNAPLGPOFP 17

RESULT 3
ID Q9BEP1 PRELIMINARY; PRT; 142 AA.
AC Q9BEP1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (Fragment).
GN TYR.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY012016; AAG38759.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
```

```
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
FT NON_TER 142
FT NON_TER 142
SQ SEQUENCE 142 AA; 16156 MW; CEADDB3FD120F7A2 CRC64;

Query Match 100.0%; Score 79; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPOFP 15
Db 3 QNILLSNAPLGPOFP 17

RESULT 4
ID Q9GLU6 PRELIMINARY; PRT; 388 AA.
AC Q9GLU6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183601; AAG27271.1; -.
DR EMBL; AF183599; AAG27271.1; JOINED.
DR EMBL; AF183600; AAG27271.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PRINTS; PR00092; TYROSINASE.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
KW Oxidoreductase.
FT NON_TER 388
FT NON_TER 388
SQ SEQUENCE 388 AA; 43807 MW; 98569EC1A450F62E CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPOFP 15
Db 56 QNILLSNAPLGPOFP 70

RESULT 5
ID Q9GLS8 PRELIMINARY; PRT; 388 AA.
AC Q9GLS8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
```

01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OS Pygathrix nemaeus (Dove langur).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Pygathrix.  
 OX NCBI\_TaxID=54133;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183656; AAG27282.1; JOINED.  
 DR EMBL; AF183654; AAG27282.1; JOINED.  
 DR EMBL; AF183655; AAG27282.1; JOINED.  
 DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR008922; Di-copper\_centre.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR Pfam; PF00264; Tyrosinase; 1.  
 DR PRINTS; PR00092; TYROSINASE.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1.  
 DR PROSITE; PS00497; TYROSINASE\_1; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 388  
 SQ SEQUENCE 388 AA; 43676 MW; 2F109910CE6D9A77 CRC64;  
 Query Match 100.0%; Score 79; DB 6; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQPP 15  
 DB 56 QNILLSNAPLGQPP 70  
 RESULT 6  
 Q9GLT6 PRELIMINARY; PRT; 388 AA.  
 AC Q9GLT6;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE Tyrosinase (Fragment).  
 OS Pygathrix avunculus (Tonkin snub-nosed monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Pygathrix.  
 OX NCBI\_TaxID=66062;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183636; AAG27274.1; JOINED.  
 DR EMBL; AF183634; AAG27274.1; JOINED.  
 DR EMBL; AF183635; AAG27274.1; JOINED.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR008922; Di-copper\_centre.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR Pfam; PF00264; Tyrosinase; 1.  
 DR PRINTS; PR00092; TYROSINASE.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1.

DR PROSITE; PS00497; TYROSINASE\_1; 1.  
 FT NON\_TER 388  
 SQ SEQUENCE 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;  
 Query Match 100.0%; Score 79; DB 6; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQPP 15  
 DB 56 QNILLSNAPLGQPP 70  
 RESULT 7  
 Q9GLV0 PRELIMINARY; PRT; 388 AA.  
 AC Q9GLV0;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183590; AAG26322.1; JOINED.  
 DR EMBL; AF183588; AAG26322.1; JOINED.  
 DR EMBL; AF183589; AAG26322.1; JOINED.  
 DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR008922; Di-copper\_centre.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR Pfam; PF00264; Tyrosinase; 1.  
 DR PRINTS; PR00092; TYROSINASE.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1.  
 DR PROSITE; PS00497; TYROSINASE\_1; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 388  
 SQ SEQUENCE 388 AA; 43865 MW; 168AECF17CC5C52B CRC64;  
 Query Match 100.0%; Score 79; DB 6; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQPP 15  
 DB 56 QNILLSNAPLGQPP 70  
 RESULT 8  
 Q9GLV2 PRELIMINARY; PRT; 388 AA.  
 AC Q9GLV2;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OS Papio hamadryas (Hamadryas baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Papio.  
 OX NCBI\_TaxID=9557;  
 RN [1]

```

RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183585; AAG21892.1; -.
DR EMBL; AF183583; AAG21892.1; JOINED.
DR EMBL; AF183584; AAG21892.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; Tyrosinase; 1.
DR PROSITE; PS00092; TYROSINASE_1.
DR PROSITE; PS00022; EGF_1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
KW Oxidoreductase.
FT NON_TER 388
SQ SEQUENCE 388 AA; 43728 MW; A6B7D85119D536FA CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15
DB 56 QNILLSNAPLGQPP 70

RESULT 9
Q9GLS4
ID Q9GLS4 PRELIMINARY; PRT; 388 AA.
AC Q9GLS4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Pygathrix roxellana (golden snub-nosed monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61522;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183671; AAG29589.1; -.
DR EMBL; AF183669; AAG29589.1; JOINED.
DR EMBL; AF183670; AAG29589.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; Tyrosinase; 1.
DR PROSITE; PS00092; TYROSINASE.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
KW Oxidoreductase.
FT NON_TER 388
SQ SEQUENCE 388 AA; 43646 MW; 73A2F0209EC377BC CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15
DB 56 QNILLSNAPLGQPP 70

RESULT 10
Q9GKM6
ID Q9GKM6 PRELIMINARY; PRT; 388 AA.
AC Q9GKM6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Macaca thibetana (Pere David's macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=54602;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183659; AAG42044.1; -.
DR EMBL; AF183660; AAG42044.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; Tyrosinase; 1.
DR PROSITE; PS00092; TYROSINASE.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
KW Oxidoreductase.
FT NON_TER 388
SQ SEQUENCE 388 AA; 43718 MW; 1196D52193651044 CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15
DB 56 QNILLSNAPLGQPP 70

RESULT 11
Q9GLS0
ID Q9GLS0 PRELIMINARY; PRT; 388 AA.
AC Q9GLS0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Trachypithecus leucocephalus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61617;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183681; AAG33680.1; -.

```



```

DR EMBL; AF183679; AAG33680.1; JOINED.
DR EMBL; AF183680; AAG33680.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PRINTS; PS00092; TYROSINASE.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
DR Oxidoreductase.
KW NON TER 388
SQ SEQUENCE 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPPF 15
DB 56 QNILLSNAPLGQPPF 70

RESULT 12
Q9GLS6 PRELIMINARY; PRT; 388 AA.
ID Q9GLS6
AC Q9GLS6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment)
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Trachypithecus.
NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183666; AAG29587.1; JOINED.
DR EMBL; AF183664; AAG29587.1; JOINED.
DR EMBL; AF183665; AAG29587.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PRINTS; PS00092; TYROSINASE.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
DR Oxidoreductase.
KW NON TER 388
SQ SEQUENCE 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPPF 15
DB 56 QNILLSNAPLGQPPF 70

RESULT 13
Q9GLS2 PRELIMINARY; PRT; 388 AA.
ID Q9GLS2
AC Q9GLS2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment)
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Trachypithecus.
NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183676; AAG33678.1; JOINED.
DR EMBL; AF183674; AAG33678.1; JOINED.
DR EMBL; AF183675; AAG33678.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PRINTS; PS00092; TYROSINASE.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
DR Oxidoreductase.
KW NON TER 388
SQ SEQUENCE 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPPF 15
DB 56 QNILLSNAPLGQPPF 70

RESULT 14
Q9GLV4 PRELIMINARY; PRT; 388 AA.
ID Q9GLV4
AC Q9GLV4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment)
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183580; AAG26320.1; JOINED.
DR EMBL; AF183578; AAG26320.1; JOINED.
DR EMBL; AF183579; AAG26320.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.

```

Search completed: June 3, 2004, 15:14:11  
Job time : 37.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:23 ; Search time 50 Seconds  
(without alignments)  
84.764 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70

Perfect score: 79

Sequence: 1 QNILLSNAPLGPQPP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: \_geneseqp1980s:\*  
2: \_geneseqp1990s:\*  
3: \_geneseqp2000s:\*  
4: \_geneseqp2001s:\*  
5: \_geneseqp2002s:\*  
6: \_geneseqp2003as:\*  
7: \_geneseqp2003bs:\*  
8: \_geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	2	AAW15321 Class II
2	79	100.0	15	2	AAW71591 Class II
3	79	100.0	15	2	AAW85296 Helper T-
4	79	100.0	15	2	AAI40209 Amino aci
5	79	100.0	15	2	AAI33168 Human tyr
6	79	100.0	15	2	AAI26865 Melanoma-
7	79	100.0	15	2	AAI00710 Tumour an
8	79	100.0	15	2	AAI49658 Tumour an
9	79	100.0	15	2	AAI01748 Exemplary
10	79	100.0	15	3	AAI71515 Human tyr
11	79	100.0	15	3	AAI33739 Peptide f
12	79	100.0	15	3	AAI92295 Tyrosinas
13	79	100.0	15	3	AAI84291 Tumour as
14	79	100.0	15	3	AAI82974 Tyrosinas
15	79	100.0	15	3	AAI02617 Tumour as
16	79	100.0	15	3	AAI08689 Antigenic
17	79	100.0	15	4	AAI99392 Vaccine r
18	79	100.0	15	4	AAI02106 Tyrosinas
19	79	100.0	15	4	AAI31349 Exemplary
20	79	100.0	15	4	AAI06836 Human tyr
21	79	100.0	15	5	ABG79139 Human tyr
22	79	100.0	15	5	AAI19078 HLA-DR4 r
23	79	100.0	15	5	AAI19543 Human can
24	79	100.0	30	5	AAU84892 Human tyr
25	79	100.0	273	2	AAI48368 Human tyr

26	79	100.0	508	2	AAW38167 Mutant hu
27	79	100.0	529	2	AAI56309 Human tyr
28	79	100.0	529	2	AAI63623 Human tyr
29	79	100.0	529	2	AAW00184 Human tyr
30	79	100.0	529	2	AAW03306 Tyrosinas
31	79	100.0	529	2	AAW38166 Normal hu
32	79	100.0	529	2	AAW36519 Tyrosinas
33	79	100.0	529	2	AAW71234 Tyrosinas
34	79	100.0	529	4	AAI51344 Human tyr
35	79	100.0	529	4	AAI86039 Human tyr
36	79	100.0	529	5	AAU84806 Human tyr
37	79	100.0	529	5	AAU11544 Human mel
38	79	100.0	529	6	ABP74129 Human tyr
39	79	100.0	529	6	ABR83439 Human tyr
40	79	100.0	529	7	ADC09566 Tyrosinas
41	79	100.0	531	2	AAI07071 Sequence
42	79	100.0	531	2	AAI79493 Human tyr
43	79	100.0	531	2	AAW22083 Human SK2
44	79	100.0	560	2	AAW38165 Human tyr
45	79	100.0	5546	5	AAU85008 Human mel

## ALIGNMENTS

RESULT 1  
AAW15321  
ID AAW15321 standard; peptide; 15 AA.

AC AAW15321;

DT 09-FEB-1998 (first entry)

DE Class II restricted melanoma tyrosinase derived antigenic peptide 1.

XX Major histocompatibility complex; MHC; Class II; tyrosinase; vaccine;  
immune response; immunogenic peptide; melanoma; treatment;  
protective antibody; immune cells; CD8+ T cell; CD4+ T cell.

OS Synthetic.

OS Homo sapiens.

PN WO9711669-A2.

XX 03-APR-1997.

XX 25-SEP-1996; 96WO-US015346.

XX 26-SEP-1995; 95US-00533895.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Topalian SL, Rosenberg SA, Robbins PF;

WPI; 1997-212652/19.

PT Major histocompatibility complex Class H immunogenic peptide - used to  
prevent or treat melanoma in mammal by stimulating production of  
protective antibodies or immune cells.

Claim 2; Page 59; 79pp; English.

XX Peptides AAW15321-56 are major histocompatibility complex (MHC) Class II  
restricted melanoma peptides, derived from tyrosinase. Tumour reactive  
human CD4+ and CD8+ T cells recognise melanoma antigens encoded by the  
tyrosinase gene. The present sequence is derived from amino acids 56-70.  
The peptides may be used as a vaccine, either prophylactically in advance  
of any evidence of melanoma, or therapeutically to enhance the patient's  
own immune response. The immunogenic peptides can be used to prevent or  
treat melanoma in a mammal by stimulating the production of protective  
antibodies or immune cells, preferably immune positive CD4+ T cells

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
 DB 1 QNILLSNAPLGQFPF 15

RESULT 2  
 AAW71591  
 ID AAW71591 standard; peptide; 15 AA.  
 AC AAW71591;  
 XX  
 XX  
 XX  
 DT 24-NOV-1998 (first entry)  
 XX  
 DE Class II-restricted epitope.  
 XX  
 KW Hepatitis B surface antigen; HBsAg; MHC class II-restricted peptide;  
 KW vaccination; vaccine; MHC class I molecule; immune response; cancer;  
 KW major histocompatibility complex molecule; pathogenic organism;  
 KW viral disease; autoimmune condition; allergy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9833523-A1.  
 XX  
 XX  
 PD 06-AUG-1998.  
 XX  
 XX  
 PF 02-FEB-1998; 98WO-GB000325.  
 XX  
 PR 31-JAN-1997; 97GB-00001999.  
 PR 05-JUL-1997; 97GB-00014182.  
 PR 07-AUG-1997; 97GB-00016620.  
 PR 07-AUG-1997; 97GB-00016641.  
 PR 21-NOV-1997; 97GB-00024584.  
 XX  
 XX (BIOV-) BIOVATION LTD.  
 PA  
 XX Carr FU, Carter G;  
 PI WPI; 1998-437178/37.  
 XX  
 DR  
 XX  
 PT Immunogenic molecules - comprising nucleic acid and polypeptide portion,  
 PT from both of which peptide for presentation on major histocompatibility  
 PT complex molecules can be derived.  
 XX  
 PS Example 5; Page 49; 87pp; English.  
 XX  
 CC A molecule has been developed which comprises: (a) a nucleic acid portion  
 CC from which at least one peptide for presentation of MHC class I or class  
 CC II molecules, or both, may be derived, and (b) a polypeptide portion,  
 CC from which at least 1 peptide for presentation on MHC class I or class II  
 CC molecules, or both, may be derived. Also described in the present  
 CC invention is another molecule comprising: (a) a nucleic acid portion from  
 CC which at least 1 peptide for presentation on MHC class I or class II  
 CC molecules, or both, may be derived, and (b) a polypeptide portion  
 CC comprising a recognition domain capable of targeting the molecule to an  
 CC antigen presenting cell (APC), where the polypeptide portion does not  
 CC comprise a specific antigen binding site. The molecules can be used to  
 CC induce immune responses to treat or prevent, e.g. diseases caused by  
 CC pathogenic organisms, cancers, viral disease, e.g. HIV or hepatitis  
 CC infection, autoimmune conditions, e.g. Grave's disease, multiple  
 CC sclerosis, systemic lupus erythematosus, diabetes mellitus, Kawasaki's  
 CC allergic rhinitis, allergic conjunctivitis, atopic asthma or eczema. The  
 CC combination of DNA and polypeptide in the same molecule can give rise not  
 CC only to a combination of MHC class I- and MHC class II-mediated immune  
 CC responses but also to an enhancement of these responses compared to the  
 CC responses given by either DNA or polypeptide alone. The present sequence  
 CC represents an epitope used in an example from the present invention

XX Sequence 15 AA;  
 SQ  
 Query Match 100.0%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
 DB 1 QNILLSNAPLGQFPF 15

RESULT 3  
 AAW85296  
 ID AAW85296 standard; peptide; 15 AA.  
 XX  
 AC AAW85296;  
 XX  
 XX  
 DT 16-FEB-1999 (first entry)  
 XX  
 DE Helper T-cell class II peptide derived from a tyrosinase.  
 XX  
 KW Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;  
 KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;  
 KW acquired immune deficiency syndrome; malaria; cancer;  
 KW allograft rejection; allergy; Lyme disease; hepatitis;  
 KW post-streptococcal endocarditis; glomerulonephritis;  
 KW food hypersensitivity.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9832456-A1.  
 XX  
 PD 30-JUL-1998.  
 XX  
 PR 23-JAN-1998; 98WO-US001373.  
 XX  
 PR 23-JAN-1997; 97US-0036713P.  
 PR 07-FEB-1997; 97US-0037432P.  
 XX  
 XX (EPIM-) EPIMUNE INC.  
 PA  
 XX Sette A, Sidney J, Southwood S;  
 PI WPI; 1998-427679/36.  
 XX  
 DR  
 XX Composition containing peptide that induces cytotoxic T lymphocyte  
 PT response, and helper peptide - can bind to human leucocyte antigen  
 PT alleles, used to treat or prevent cancers, parasitic infections and  
 PT autoimmune disease.  
 XX  
 PS Disclosure; Page 40; 51pp; English.  
 XX  
 CC AAW85284-451 represent helper T-cell class II peptides, which can bind to  
 CC the human leucocyte antigens (HLA) DR4w4, DR1 and DR7. The peptides are  
 CC used in the course of the invention. The specification describes peptides  
 CC that that induce a cytotoxic T lymphocyte (CTL) response, and T-helper  
 CC peptides, that are used together to generate a CTL response for the  
 CC treatment or prevention of viral, fungal, bacterial or parasitic  
 CC infections (e.g. hepatitis, acquired immune deficiency syndrome or  
 CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate  
 CC cancer or condyloma acuminatum). Helper T-cell peptides may be used alone  
 CC to induce a helper T cell response, e.g. in cases of autoimmune disease,  
 CC allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal  
 CC endocarditis, glomerulonephritis and food hypersensitivity  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15



DT 14-SEP-1999 (first entry)  
 XX Melanoma-derived lipopeptide epitope #6 for mixed micelles.  
 DE  
 XX  
 XX Micelle; microaggregate; induction; immune response; lipopeptide; CTL;  
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;  
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;  
 KW melanoma; Plasmodium falciparum; malaria.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 OS  
 XX FR2771640-A1.  
 XX  
 XX 04-JUN-1999.  
 XX  
 XX 03-DEC-1997; 97FR-00015246.  
 PF  
 XX 03-DEC-1997; 97FR-00015246.  
 PR  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX PA (INSP ) INST PASTEUR LILLE.  
 XX  
 XX Gras MH, Bossus M, Lippens G, Wieruszski JM, Tartar A;  
 PI Guillet JG, Bourgault VI;  
 XX WPI; 1999-349509/30.  
 XX  
 XX Immunogenic lipopeptide micelles - comprising lipopeptides containing  
 PT cytotoxic and helper T-lymphocyte epitopes.  
 PT  
 XX Disclosure; Page 37; 60pp; French.  
 PS  
 XX The invention relates to the generation of mixed micelles or  
 CC microaggregates for inducing an immune response comprise: (a) a first  
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope  
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at  
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit  
 CC different from that of the first lipopeptide. This peptide represents an  
 CC example of a lipopeptide epitope used in the invention and is derived  
 CC from a human melanoma protein. The immunogenic lipopeptide micelles are  
 CC used in vaccines, especially against HIV, hepatitis B virus (HBV),  
 CC papilloma viruses, p53, melanoma or Plasmodium falciparum malaria  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 100.0%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 QNILLSNAPLGQFPF 15  
 DB 1 QNILLSNAPLGQFPF 15  
 RESULT 7  
 AAY00710  
 ID AAY00710 standard; peptide; 15 AA.  
 XX  
 AC AAY00710;  
 XX  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE Tumour antigen booster peptide Tyrosinase HLA-DR4.  
 XX  
 KW Tumour antigen; booster peptide; immune response modulation; allergy;  
 KW immune response enhancer; tumour cell; tumour rejection antigen;  
 KW leukocyte antigen-presenting molecule; autoimmune disease;  
 KW allograft rejection.  
 XX  
 OS Homo sapiens.  
 OS  
 XX

PN WO9858956-A2.  
 XX  
 PD 30-DEC-1998.  
 XX  
 PF 19-JUN-1998; 98WO-US012894.  
 XX  
 PR 23-JUN-1997; 97US-00880979.  
 XX  
 PA (LUDM-) LUDWIG INST CANCER RES.  
 XX  
 XX Warnier G, Uyttenhove C, Boon-Falleur T;  
 PI WPI; 1999-105612/09.  
 XX  
 XX Immunization methods using viruses expressing antigen for priming and  
 PT booster immunizations - useful for modulating immune responses against  
 PT antigen, e.g. enhancing immune response against tumour cells expressing  
 PT tumour rejection antigens.  
 XX  
 PS Disclosure; Page 9; 33pp; English.  
 XX  
 CC This sequence represents a tumour antigen booster peptide that can be  
 CC used in the method of the invention. The method is for for modulating an  
 CC immune response in a mammal against an antigen, and comprises: (A)  
 CC inducing an immune response by: (i) administering a virus containing a  
 CC nucleic acid molecule encoding the antigen or its precursor to generate  
 CC an immune response; and (ii) administering at least one booster dose  
 CC comprising a peptide including the antigen, in an adjuvant, in a combined  
 CC amount effective to enhance the initial immune response; or (B) reducing  
 CC an immune response as defined for (A) but using a non-adjuvant with the  
 CC peptide which includes the antigen, in an amount effective to reduce the  
 CC initial immune response. Method (A) is used to enhance the immune  
 CC response against tumour cells expressing tumour rejection antigens, and  
 CC against pathogens in subjects having human leukocyte antigen-presenting  
 CC molecules. Method (B) is used to reduce the immune response in allergy,  
 CC autoimmune disease, and allograft rejection. Method (A) provides an  
 CC immunisation method which, unlike prior art, is not limited by the host  
 CC immune response against viral vectors  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 QNILLSNAPLGQFPF 15  
 DB 1 QNILLSNAPLGQFPF 15  
 RESULT 8  
 AAY49658  
 ID AAY49658 standard; peptide; 15 AA.  
 XX  
 AC AAY49658;  
 XX  
 DT 14-JAN-2000 (first entry)  
 XX  
 DE Tumour antigenic peptide SEQ ID NO:25.  
 XX  
 KW Human; sdp3.10; SAGE; sdp3.8; HAGE; sdp3.5; TRAP; sarcoma;  
 KW tumour rejection antigen precursor; tumour associated nucleic acid;  
 KW carcinoma; cancer; immune response; diagnosis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9953061-A2.  
 XX  
 PD 21-OCT-1999.  
 XX  
 PF 14-APR-1999; 99WO-US008163.  
 XX  
 XX 15-APR-1998; 98US-00060706.

PR 27-JUL-1998; 98US-00122989.  
 PR 30-OCT-1998; 98US-00183706.  
 PR 30-OCT-1998; 98US-00183799.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Martelange V, De Smet C, Boon-Falleur T;  
 XX WPI; 1999-620430/53.  
 XX New nucleic acid encoding sarcoma-associated gene products, useful for  
 PT diagnosing, e.g. treating and preventing cancer.  
 PT Disclosure; Page 25; 93pp; English.  
 XX The present invention describes sarcoma-associated gene products (I).  
 CC Agents, specifically sarcoma associated nucleic acids (II) or their  
 CC expression products that are tumour rejection antigens (TRA), that  
 CC selectively increase formation of HLA (human leucocyte antigen)/(I)  
 CC complexes are used for treating cancer, especially sarcoma and carcinoma,  
 CC in humans and other animals. Compositions containing autologous cytolytic  
 CC T cells (CTL), specific for the HLA/(I) complex, are similarly useful,  
 CC also transformed cells that stimulate such CTL in vivo. (III) are also  
 CC used: (i) as source of therapeutic antisense sequences that reduce  
 CC expression of (II); (ii) for recombinant production of (I); (iii)  
 CC particularly its fragments, as primers and probes in usual hybridisation  
 CC and amplification assays, for diagnosis, prognosis and monitoring of  
 CC tumours, or for measuring binding specificity of HLA molecules or CTL  
 CC clones; (iv) to identify related sequences; and (v) for generating  
 CC transgenic animals, e.g. for studying cancer and immune responses to it.  
 CC (I) are used to raise specific antibodies (Ab) and therapeutically. Ab  
 CC are used to diagnose tumours in immunoassays, also for delivering drugs,  
 CC toxins, imaging agents etc. to (I)-expressing cells. AAY49637 to AAY49670  
 CC represent exemplary tumour antigenic peptides given in the present  
 CC invention  
 XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQPPF 15  
 Db 1 QNILLSNAPLGQPPF 15  
 RESULT 9  
 AAY01748  
 ID AAY01748 standard; peptide; 15 AA.  
 XX AC AAY01748;  
 XX DT 25-JUN-1999 (first entry)  
 XX DE Exemplary antigenic peptide derived from Tyrosinase.  
 XX KW MAGE-3; tumour associated gene; human leucocyte antigen Class II;  
 KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;  
 KW osteosarcoma; leukemia; carcinoma.  
 XX OS Homo sapiens.  
 XX PN WO9914326-A1.  
 XX PD 25-MAR-1999.  
 XX PF 04-SEP-1998; 98WO-US018601.  
 XX PR 12-SEP-1997; 97US-00928615.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA (UYVR-) UNIV VRIJE BRUSSEL.

XX Thielemans K, Heirman C, Corthals J, Chau P, Stroobant V;  
 PI Boon-Falleur T, Van Der Bruggen P, Luiten R;  
 XX WPI; 1999-244031/20.  
 XX Isolated peptides that bind to human leucocyte antigen class II  
 PT molecules.  
 XX Disclosure; Page 29; 88pp; English.  
 XX The present sequence represents an exemplary tumour associated peptide  
 CC antigen. The specification describes a MAGE-3 tumour associated gene.  
 CC Peptides (AAY01721-25) that bind human leucocyte antigen (HLA) class II  
 CC molecules can be derived from the MAGE-3 protein. These peptides and  
 CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide and HLA  
 CC Class II, are used to treat MAGE-3 related diseases, particularly cancers  
 CC (e.g. melanoma, osteosarcoma, leukemia and various forms of carcinoma).  
 CC The peptides are also used to produce specific antibodies. Detection of  
 CC of the peptides, e.g. in binding assays, particularly with antibodies, is  
 CC used for diagnosis of such diseases  
 XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQPPF 15  
 Db 1 QNILLSNAPLGQPPF 15  
 RESULT 10  
 AAY71515  
 ID AAY71515 standard; peptide; 15 AA.  
 XX AC AAY71515;  
 XX DT 12-OCT-2000 (first entry)  
 XX DE Human Tyrosinase peptide-5.  
 XX KW Tyrosinase; human; Tumour Rejection Antigen; TRA; tumour; cancer; HLA;  
 KW Human Leucocyte Antigen; MHC; Major Histocompatibility Complex; CTL;  
 KW cytolytic T-lymphocyte; immune response stimulator; prophylaxis; therapy;  
 KW diagnosis; TNF; tumour necrosis factor; vaccine; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO200032769-A2.  
 XX PD 08-JUN-2000.  
 XX PF 26-NOV-1999; 99WO-IB002018.  
 XX PR 27-NOV-1998; 98GB-00026143.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;  
 PI WPI; 2000-412317/35.  
 XX DR Novel polypeptides expressed in tumor cells useful for treating cancers  
 PT have an ability to complex with a major histocompatibility complex  
 PT molecule and comprises a specific unbroken amino acid sequence.  
 XX Disclosure; Page 19; 80pp; English.  
 XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and  
 CC decapeptide sequences, that function as tumour rejection antigens (TRAs).  
 CC These peptides are capable of forming a complex with major

CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte  
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune  
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune  
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,  
 CC therapy and diagnosis of tumours and are effective in controlling or  
 CC preventing tumour growth. The present sequence is the human Tyrosinase  
 CC peptide-5, that corresponds to residues 56-70 of the tumour associated  
 CC gene, tyrosinase encoding protein. It can be administered to induce or  
 CC enhance an immune response and is presented by HLA-DR4 complex. This  
 CC peptide can serve as a tumour rejection antigen (TRA) and in combination  
 CC with adjuvants, can produce vaccines useful for treating a variety of  
 CC tumours  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
 Db 1 QNILLSNAPLGQPP 15

RESULT 11  
 AAB13739  
 ID AAB13739 standard; peptide; 15 AA.

XX AAB13739;

XX 02-FEB-2001 (first entry)

XX Peptide fragment # 5 from human tyrosinase.

XX Human; T-cell; immune response; antigen; epitope; B7 family molecule;  
 KW Leukocyte function-associated antigen-3; LFA-3;  
 KW Interleukin adhesion molecule-1; ICAM-1; vaccine; immunotherapy;  
 KW colon poly; Crohn's disease; ulcerative colitis; breast lesion; tumour;  
 KW tyrosinase.

XX Homo sapiens.

XX WO200034494-A1.

XX 15-JUN-2000.

XX 12-NOV-1999; 99WO-US026866.

XX 09-DEC-1998; 98US-0111582P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX (THER-) THERION BIOLOGICS CORP.

XX Schlom J, Hodge J, Panicali D;

XX WPI; 2000-431307/37.

XX Novel recombinant vector useful as immunogens and vaccines for  
 PT stimulating and enhancing immunological responses to target cells and  
 PT antigens expresses multiple co-stimulatory molecules such as B7-1, LFA-3,  
 PT ICAM-1.

XX Claim 18; Page 35; 188pp; English.

XX Costimulatory molecules have important roles in T-cell activation and  
 CC therefore the immune response. The present invention relates to  
 CC recombinant vectors which comprise of foreign nucleic acid sequences  
 CC encoding at least three costimulatory molecules: a B7 family molecule,  
 CC Leukocyte function-associated antigen-3 (LFA-3, human CD58) and  
 CC Interleukin adhesion molecule-1 (ICAM-1, CD54) and optionally a foreign  
 CC gene encoding a target antigen or immunological epitope. The present  
 CC sequence is one such target antigen used in the present invention. The  
 CC present sequence is a tumour-associated antigen. The vector of the

CC present invention would be useful for providing an enhanced immune  
 CC response to the present target antigen. The vector of the present  
 CC invention may therefore be useful in immunotherapy for treating or  
 CC preventing diseases caused by viruses, bacteria, protozoans, parasites,  
 CC premalignant cells and tumour cells. The recombinant vector can be used  
 CC to treat or prevent preneoplastic or hyperplastic states such as colon  
 CC polyps, Crohn's disease, ulcerative colitis and breast lesions  
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
 Db 1 QNILLSNAPLGQPP 15

RESULT 12

AA92295

ID AA92295 standard; peptide; 15 AA.

XX AA92295;

XX 10-AUG-2000 (first entry)

XX Tyrosinase antigenic peptide epitope (residues 56-70).

XX Tyrosinase; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;  
 KW human leukocyte antigen; HLA.

XX Homo sapiens.

XX WO200020445-A2.

XX 13-APR-2000.

XX 15-SEP-1999; 99WO-IB001664.

XX 02-OCT-1998; 98US-00165863.

XX 09-APR-1999; 99US-00289350.

XX (CHAU/) CHAU P.

XX (LUIT/) LUITEN R.

XX (DEMO/) DEMOTTE N.

XX (DUFE/) DUFFOUR M.

XX (LURQ/) LURQUIN C.

XX (TRAV/) TRAVERSARI C.

XX (STRO/) STROOBANT V.

XX (CORN/) CORNELIS G R.

XX (BOON/) BOON-FALLEUR T.

XX (VERU/) VAN DER BRUGGEN P.

XX (SCHU/) SCHULTZ E.

XX (WARN/) WARNIER G.

XX Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;  
 PI Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;  
 PI Schultz E, Warnier G;

XX WPI; 2000-303739/26.

XX Isolation of cytotoxic T-lymphocytes clones by successive steps of  
 PT stimulation and testing of lymphocytes with antigen presenting cells  
 PT which present antigens derived from different expression systems.

XX Disclosure; Page 22; 99pp; English.

XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones  
 CC comprises successive steps of stimulation and testing of lymphocytes with  
 CC antigen presenting cells (APCs) which present antigens derived from  
 CC different expression systems. The CTL clones isolated recognize specific  
 CC antigenic peptides of proteins, preferably of the MAGE family. The APC is



CC autologous and each expression systems is different from at least one of  
CC the other expression systems, therefore isolating a cytotoxic T cell  
CC clone specific for the protein. The method can also be used to identify  
CC an antigenic peptide epitope. Isolated CTL clones specific for a  
CC peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells  
CC specific for the complexes, peptides or cells which present the complexes  
CC on the cell surface are useful for treating pathological conditions  
CC characterized by abnormal expression of the complexes  
XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPP 15  
| | | | | | | | | | | | | | |  
Db 1 QNILLSNAPLGQPP 15

## RESULT 13

RAY84291  
ID AAY84291 standard; peptide; 15 AA.

XX AC AAY84291;  
XX DT 12-JUL-2000 (first entry)  
XX DE Tumour associated antigen derived from tyrosinase.  
XX KW tumour rejection antigen; macrophage colony stimulating gene;  
XX KW macrophage-colony stimulating factor; antigen presenting cell;  
XX KW human leukocyte antigen; CD8+ cytotoxic T lymphocyte.  
XX OS Homo sapiens.  
XX PN WO200013699-A1.  
XX PD 16-MAR-2000.

PF 03-SEP-1999; 99WO-US020344.

PR 04-SEP-1998; 98US-0099077P.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Probst-Kepper M, Van Den Eynde B, Boon-Falleur T;

XX WPI; 2000-256859/22.

PT Isolated polypeptide used to treat subjects having a disorder  
PT characterized by expression of alternative open reading frame macrophage-  
PT colony stimulating factor comprises 25 amino acid residue sequence.

PS Disclosure; Page 20; 74pp; English.

XX AAY84270-Y84303 represent peptides which are tumour associated antigens.  
CC They can be administered in conjunction with the tumour rejection antigen.  
CC precursor of the invention to induce anti-tumour responses. The tumour  
CC rejection antigen precursor of the invention is encoded by an alternative  
CC open reading frame (ORF) of human macrophage colony stimulating gene.  
CC peptides derived from the alternative ORF of macrophage-colony  
CC stimulating factor, when presented by an antigen presenting cell having a  
CC human leukocyte antigen (HLA) class I molecule, effectively induce the  
CC activation and proliferation of CD8+ cytotoxic T lymphocytes. Polypeptide  
CC and nucleic acids derived from the alternate ORF of macrophage-colony  
CC stimulating factor are useful for enriching selectively a population of T  
CC lymphocytes with CD8+ T lymphocytes. They are also useful for diagnosing  
CC a disorder characterized by expression of the polypeptide, and for  
CC identifying functional variants and mimetics

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPP 15  
| | | | | | | | | | | | | | |  
Db 1 QNILLSNAPLGQPP 15

## RESULT 14

AAY82974  
ID AAY82974 standard; peptide; 15 AA.

XX AC AAY82974;

XX DT 19-JUN-2000 (first entry)

XX DE Tyrosinase tumour associated antigen.

XX KW Tumour; tumour associated antigen; retrovirus; antisense; treatment;  
XX KW probe; primer; HLA; cytotoxic T-lymphocyte; cancer; testis; antibody;  
XX KW CTL; helper T-lymphocyte; MAGE; BAGE; GAGE; Gnt-V; MUM; CDK4;  
XX KW beta catenin; tyrosinase; Melan-A; gp100; PRAVE.

XX OS Homo sapiens.

XX PN WO200006598-A1.

XX PD 10-FEB-2000.

XX PF 15-JUL-1999; 99WO-US016236.

XX PR 29-JUL-1998; 98US-00124398.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Coulie P, Boon-Falleur T;

XX WPI; 2000-205453/18.

XX Novel nucleic acids encoding melanoma associated gene products and their  
XX fragments and variants, useful for treating endogenous retrovirus  
XX mediated tumors, especially melanomas.

PS Disclosure; Page 26; 77pp; English.

XX Tumor associated disorders (e.g. endogenous retrovirus mediated tumors,  
XX especially melanomas) can be treated or ameliorated by administering  
XX antisense nucleic acid to reduce the expression of tumour associated  
XX genes such as HERV-AVL3-B. Progression of a disorder characterized by the  
XX expression of the HERV-AVL3-B endogenous retrovirus tumor rejection  
XX antigen (ERTRA) can be diagnosed or monitored by contacting a non-testis  
XX biological sample with an agent that binds to the complex and determining  
XX the interaction. A disorder can also be treated by administering an agent  
XX that enriches the presence of HLA and HERV-AVL3-B ERTRA or by  
XX administering autologous cytotoxic T-cells sufficient to ameliorate the  
XX disorder. Fragments of the HERV-AVL3-B coding sequence are useful as  
XX probes or amplification primers for determining the expression of HERV-  
XX AVL3-B genes, to express tumor associated polypeptides in vivo and in  
XX vitro and to prepare fragments of such polypeptides to synthesize  
XX antibodies. Antigenic peptides of HERV-AVL3-B can be useful for  
XX generating antibodies either alone or as fusion proteins, as components  
XX of immunoassay and for determining the binding specificity of HLA  
XX molecules and/or cytotoxic T lymphocyte (CTL) for HERV-AVL3-B proteins.  
XX Peptides derived from the HERV-AVL3-B coding sequence and which are  
XX presented by MHC molecules and recognised by CTL or helper T-lymphocytes  
XX can be combined with peptides from other tumour rejection antigens by  
XX preparation of hybrid nucleic acids or polypeptides to produce polytopes.  
XX This exemplary tumour associated peptide antigen corresponds to amino  
XX acids 56-70 of the tyrosinase polypeptide. See also AAY82953-Y82986

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: June 3, 2004, 15:12:45  
Job time : 51 secs

QY 1 QNILLSNAPLGQFPF 15  
DB 1 QNILLSNAPLGQFPF 15

## RESULT 15

AAB02617  
ID AAB02617 standard; peptide; 15 AA.

XX AC AAB02617;

DT 18-AUG-2000 (first entry)

XX Tumour associated peptide antigen from Tyrosinase #6.

XX KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;  
XX KW cancer; human; tumour; tumour associated gene product.

XX OS Homo sapiens.

XX PN WO200020581-A1.

XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-US021230.

XX PR 05-OCT-1998; 98US-00166448.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PA (UYVR-) UNIV VRIJE BRUSSEL.

XX PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;  
PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;  
PI Heirman C;

XX DR WPI; 2000-317713/27.

XX PT New MAGE-A3 class II binding peptides, useful to diagnose and treat  
XX PT tumors, are fragments of MAGE-A3 which bind to and are presented to T  
XX PT lymphocytes by human leukocyte antigen class II molecules.

XX PS Disclosure; Page 33; 119pp; English.

XX CC The present invention relates to MAGE-A3 (tumour associated gene product)  
XX CC human leukocyte antigen (HLA) class II-binding peptides (see AAB02566-  
XX CC B02595, and AAB02633-B02637). These peptides are presented to T cells in  
XX CC the context of HLA class II molecules. The peptides stimulate the  
XX CC activity and proliferation of CD4+ T lymphocytes. The invention also  
XX CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928 and  
XX CC AAA37938-A37940). The peptides and nucleotide sequences can be used to  
XX CC create antibodies against the MAGE-A3 peptides, the antibodies, peptides  
XX CC and nucleotide sequences can be used to create a vaccine. The peptides  
XX CC are used to diagnose or treat a disorder characterized by expression of  
XX CC MAGE-3, particularly cancer. The methods can also be used in the  
XX CC diagnosis of disorders associated with MAGE-3 expression. Included in the  
XX CC invention are other human tumour antigens (see AAB02596-B02637), and PCR  
XX CC primers used in the course of the invention (see AAA37929-A37937 and  
XX CC AAA37941-A37942)

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15

DB 1 QNILLSNAPLGQFPF 15

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:14:49 ; Search time 39 Seconds  
(without alignments)  
108.207 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70

Perfect score: 79

Sequence: 1 QNILLSNAPLGQFPF 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	15	9	US-09-923-831-25
2	79	100.0	15	9	US-09-766-889A-37
3	79	100.0	15	12	US-10-218-095-32
4	79	100.0	15	12	US-10-253-286-500
5	79	100.0	15	12	US-10-103-395-198
6	79	100.0	15	14	US-10-161-097-24
7	79	100.0	15	14	US-10-170-832-66
8	79	100.0	15	14	US-10-239-313A-495
9	79	100.0	15	15	US-10-245-871-500
10	79	100.0	15	15	US-10-406-317-13
11	79	100.0	15	16	US-10-297-168-13
12	79	100.0	20	12	US-10-253-286-503
13	79	100.0	20	15	US-10-245-871-503
14	79	100.0	30	12	US-10-296-734-978
15	79	100.0	32	12	US-10-253-286-525

16	79	100.0	32	15	US-10-245-871-525	Sequence 525, App
17	79	100.0	43	16	US-10-447-161-142	Sequence 142, App
18	79	100.0	529	12	US-10-296-734-820	Sequence 820, App
19	79	100.0	529	12	US-10-253-286-487	Sequence 487, App
20	79	100.0	529	13	US-10-011-436-4	Sequence 4, Appli
21	79	100.0	529	15	US-10-026-066-4	Sequence 2, Appli
22	79	100.0	529	15	US-10-117-937-2	Sequence 487, App
23	79	100.0	529	15	US-10-245-871-487	Sequence 1210, Ap
24	79	100.0	5546	12	US-10-296-734-1210	Sequence 506, App
25	78	98.7	15	14	US-10-239-313A-506	Sequence 493, App
26	77	97.5	15	14	US-10-239-313A-493	Sequence 497, App
27	76	96.2	15	14	US-10-239-313A-497	Sequence 503, App
28	76	96.2	15	14	US-10-239-313A-503	Sequence 505, App
29	76	96.2	15	14	US-10-239-313A-505	Sequence 481, App
30	75	94.9	15	14	US-10-239-313A-481	Sequence 492, App
31	75	94.9	15	14	US-10-239-313A-492	Sequence 494, App
32	75	94.9	15	14	US-10-239-313A-494	Sequence 500, App
33	75	94.9	15	14	US-10-239-313A-500	Sequence 496, App
34	73	92.4	15	14	US-10-239-313A-496	Sequence 502, App
35	73	92.4	15	14	US-10-239-313A-502	Sequence 504, App
36	73	92.4	15	14	US-10-239-313A-504	Sequence 498, App
37	71	89.9	15	14	US-10-239-313A-498	Sequence 499, App
38	70	88.6	15	14	US-10-239-313A-499	Sequence 41, Appl
39	66	83.5	13	9	US-09-847-185-41	Sequence 980, App
40	66	83.5	13	14	US-10-224-286-41	Sequence 75, Appl
41	64	81.0	30	12	US-10-296-734-980	Sequence 188890,
42	63	79.7	533	14	US-10-207-655-75	Sequence 72327, A
43	64	55.7	75	12	US-10-424-599-188890	Sequence 21, Appl
44	44	55.7	492	12	US-10-425-114-72327	
45	43	54.4	9	14	US-10-219-850-21	

#### ALIGNMENTS

RESULT 1  
US-09-923-831-25  
; Sequence 25, Application US/09923831  
; Patent No. US20020115142A1  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val,rie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/923,831  
; PRIOR FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 09/183,706  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-831-25

Query Match 100.0% Score 79; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
Db 1 QNILLSNAPLGQFPF 15

#### RESULT 2

US-09-766-889A-37  
; Sequence 37, Application US/09766889A  
; Patent No. US2002016465A1  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre

```

; APPLICANT: Strobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGN ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-37

Query Match      100.0%; Score 79; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QNILLSNAPLGQFPF 15
DB      1 QNILLSNAPLGQFPF 15

RESULT 3
US-10-218-095-32
; Sequence 32, Application US/10218095
; Publication No. US20040033541A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Strobant, Vincent
; APPLICANT: Russo, Vincenzo
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGN-A4 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: L00461/70137
; CURRENT APPLICATION NUMBER: US/10/218,095
; CURRENT FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-095-32

Query Match      100.0%; Score 79; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QNILLSNAPLGQFPF 15
DB      1 QNILLSNAPLGQFPF 15

RESULT 4
US-10-253-286-500
; Sequence 500, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813

```

```

; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 500
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-500

Query Match      100.0%; Score 79; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QNILLSNAPLGQFPF 15
DB      1 QNILLSNAPLGQFPF 15

RESULT 5
US-10-103-395-198
; Sequence 198, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; TITLE OF INVENTION: RESTRICTED EPITOPES
; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-198

Query Match      100.0%; Score 79; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QNILLSNAPLGQFPF 15
DB      1 QNILLSNAPLGQFPF 15

RESULT 6
US-10-161-097-24
; Sequence 24, Application US/10161097
; Publication No. US20030096404A1
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/10/161,097
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US/09/574,749

```

; FILE REFERENCE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/107,972  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: PCT/US99/26795  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/524,749  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Homo Sapiens source  
US-10-161-097-24

Query Match 100.0%; Score 79; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQPP 15  
DB 1 QNILLSNAPLGPQPP 15

RESULT 7  
US-10-170-832-66  
; Sequence 86, Application US/10170832  
; Publication No. US20030170792A1  
; GENERAL INFORMATION:  
; APPLICANT: Chau, Pascal  
; APPLICANT: Vantomme, Valerie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Corthals, Jurgen  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/10/170,832  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US/09/166,448  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-832-66

Query Match 100.0%; Score 79; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQPP 15  
DB 1 QNILLSNAPLGPQPP 15

RESULT 8  
US-10-239-313A-495  
; Sequence 495, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID

; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 495  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-495

Query Match 100.0%; Score 79; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQPP 15  
DB 1 QNILLSNAPLGPQPP 15

RESULT 9  
US-10-245-871-500  
; Sequence 500, Application US/10245871  
; Publication No. US20030235594A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2013  
; CURRENT APPLICATION NUMBER: US/10/245,871  
; CURRENT FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 500  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-245-871-500

Query Match 100.0%; Score 79; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQPP 15  
DB 1 QNILLSNAPLGPQPP 15

RESULT 10  
US-10-406-317-13  
; Sequence 13, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE  
US-10-406-317-13

Query Match 100.0%; Score 79; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPPFP 15  
Db 1 QNILLSNAPLGPPFP 15

## RESULT 11

US-10-297-168-13  
; Sequence 13, Application US/10297168  
; Publication No. US20040091995A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, Jeffrey  
; APPLICANT: GREINER, John W.  
; APPLICANT: KASS, Erik  
; APPLICANT: PANICALI, Dennis  
; TITLE OF INVENTION: RECOMBINANT NON-REPLICATING VIRUS EXPRESSING GM-CSF AND  
; TITLE OF INVENTION: USES THEREOF TO ENHANCE IMMUNE RESPONSES  
; FILE REFERENCE: 38163-0167  
; CURRENT APPLICATION NUMBER: US/10/297,168  
; PRIOR APPLICATION NUMBER: PCT/US01/19201  
; PRIOR FILING DATE: 2002-12-03  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US660/211,717  
; PRIOR FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-297-168-13

Query Match 100.0%; Score 79; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPPFP 15  
Db 1 QNILLSNAPLGPPFP 15

## RESULT 12

US-10-253-286-503  
; Sequence 503, Application US/10253286  
; Publication No. US20040058881A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2015  
; CURRENT APPLICATION NUMBER: US/10/253,286  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 503  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: II-key/tyrosinase non-overlapping hybrid peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: a-aminovaleic acid  
; FEATURE:  
; OTHER INFORMATION: C-term amidated  
US-10-253-286-503

Query Match 100.0%; Score 79; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPPFP 15  
Db 6 QNILLSNAPLGPPFP 20

## RESULT 13

US-10-245-871-503  
; Sequence 503, Application US/10245871  
; Publication No. US20030235594A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2013  
; CURRENT APPLICATION NUMBER: US/10/245,871  
; CURRENT FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 503  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: II-key/tyrosinase non-overlapping hybrid peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: a-aminovaleic acid  
; FEATURE:  
; OTHER INFORMATION: C-term amidated  
US-10-245-871-503

Query Match 100.0%; Score 79; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPPFP 15  
Db 6 QNILLSNAPLGPPFP 20

## RESULT 14

US-10-296-734-978  
; Sequence 978, Application US/10296734  
; Publication No. US20040054137A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Scott A  
; APPLICANT: Ramshaw, Ian A

; TITLE OF INVENTION: Synthetic molecules and uses therefor  
; FILE REFERENCE: Savine  
; CURRENT APPLICATION NUMBER: US/10/296,734  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: AU PQ7761/00  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 1507  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 978  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: tyros segment 4  
; US-10-296-734-978

Query Match 100.0%; Score 79; DB 12; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPFP 15  
Db 13 QNILLSNAPLGQPFP 27

RESULT 15  
US-10-253-286-525  
; Sequence 525, Application US/10253286  
; Publication No. US20040058881A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2015  
; CURRENT APPLICATION NUMBER: US/10/253,286  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 03/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 525  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Ii-key/tyrosinase non-overlapping hybrid peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: a-aminovaleric acid  
; FEATURE:  
; OTHER INFORMATION: C-term amidated  
; US-10-253-286-525

Query Match 100.0%; Score 79; DB 12; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPFP 15  
Db 18 QNILLSNAPLGQPFP 32

Search completed: June 3, 2004, 15:24:22  
Job time : 39 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 17:05:32 ; Search time 29 Seconds  
(without alignments)  
26.703 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70

Perfect score: 79  
Sequence: 1 QNILLSNAPLGQFP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pap.\*  
2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pap.\*  
3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pap.\*  
4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pap.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pap.\*  
6: /cgn2\_6/ptodata/2/iaa/backfile1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	2	US-09-036-582-22
2	79	100.0	15	3	US-09-183-706-25
3	79	100.0	15	3	US-09-183-706-25
4	79	100.0	15	4	US-09-166-448-66
5	79	100.0	15	4	US-09-567-995-25
6	79	100.0	15	4	US-09-165-863-22
7	79	100.0	15	4	US-09-009-953-198
8	79	100.0	15	4	US-09-697-884-66
9	79	100.0	15	4	US-09-289-350-22
10	79	100.0	15	4	US-09-574-749B-24
11	79	100.0	15	4	US-09-318-141-22
12	79	100.0	15	4	US-09-601-729-112
13	79	100.0	508	1	US-07-891-942G-10
14	79	100.0	529	1	US-07-891-942G-8
15	79	100.0	529	2	US-08-370-909-19
16	79	100.0	529	2	US-08-504-048-8
17	79	100.0	529	4	US-09-341-982-1
18	79	100.0	529	4	US-09-169-717E-39
19	79	100.0	529	4	US-10-011-436-4
20	79	100.0	537	3	US-08-540-922D-12
21	72	91.1	15	4	US-07-891-942G-5
22	66	83.5	13	2	US-09-169-717E-28
23	66	83.5	13	4	US-08-902-516-41
24	45	57.0	263	4	US-09-847-185-41
25	42	53.2	923	4	US-09-134-001C-4512
26	40	50.6	124	4	US-09-252-991A-27148
27	40	50.6	170	4	US-09-134-000C-4402
					Sequence 7110, Ap

28	40	50.6	347	3	US-08-857-076-100	Sequence 100, App
29	40	50.6	375	4	US-09-171-337A-7	Sequence 7, Appli
30	40	50.6	375	4	US-09-631-022-7	Sequence 7, Appli
31	39	49.4	563	4	US-09-252-991A-28458	Sequence 28458, A
32	39	49.4	3174	2	US-08-477-451-3	Sequence 3, Appli
33	38	48.1	280	4	US-09-489-039A-9657	Sequence 9657, Ap
34	38	48.1	370	6	5240706-5	Patent No. 5240706
35	38	48.1	441	4	US-09-489-039A-10091	Sequence 10091, A
36	38	48.1	466	1	US-08-785-066-2	Sequence 2, Appli
37	38	48.1	466	3	US-09-007-355-2	Sequence 2, Appli
38	38	48.1	466	3	US-08-913-489-2	Sequence 2, Appli
39	38	48.1	966	1	US-08-571-758-2	Sequence 2, Appli
40	38	48.1	966	1	US-08-909-984A-2	Sequence 2, Appli
41	38	48.1	966	1	US-08-909-983-2	Sequence 2, Appli
42	38	48.1	1113	4	US-09-618-425-9	Sequence 9, Appli
43	37.5	47.5	347	4	US-09-252-991A-19789	Sequence 19789, A
44	37	46.8	60	4	US-09-205-258-1084	Sequence 1084, Ap
45	37	46.8	153	3	US-09-154-083-12	Sequence 12, Appli

## ALIGNMENTS

RESULT 1  
US-09-036-582-22  
Sequence 22, Application US/09036582A  
Patent No. 5965381  
GENERAL INFORMATION:  
APPLICANT: van der Bruggen, Pierre  
APPLICANT: Cornelis, Guy R.  
TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
FILE REFERENCE: 11154  
CURRENT APPLICATION NUMBER: US/09/036,582A  
CURRENT FILING DATE: 1998-03-06  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 22  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Human Tyrosinase peptide  
US-09-036-582-22

Query Match 100.0%; Score 79; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
DB 1 QNILLSNAPLGQFP 15

RESULT 2  
US-09-183-706-25  
Sequence 25, Application US/09183706  
Patent No. 6245525  
GENERAL INFORMATION:  
APPLICANT: Martelange, Valrie  
APPLICANT: De Smet, Charles  
APPLICANT: Boon-Fallieur, Thierry  
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
FILE REFERENCE: L0461/7054  
CURRENT APPLICATION NUMBER: US/09/183,706  
CURRENT FILING DATE: 1998-10-30  
EARLIER APPLICATION NUMBER: 09/122,989  
EARLIER FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 43  
SEQ ID NO 25  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-183-706-25



Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

## RESULT 3

US-09-166-448-66 OK  
; Sequence 66, Application US/09166448  
; Patent No. 6291430  
; GENERAL INFORMATION:  
; APPLICANT: Chauv. Pascal  
; APPLICANT: Vantomme, Valrie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Corthals, Jorgen  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/09/166,448  
; CURRENT FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-166-448-66

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

## RESULT 4

US-09-567-995-25 OK  
; Sequence 25, Application US/09567995  
; Patent No. 6303756  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val,rie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/567,995  
; CURRENT FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: 09/183,706  
; PRIOR FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-567-995-25

Query Match 100.0%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

## RESULT 5

US-09-165-863-22 OK  
; Sequence 22, Application US/09165863  
; Patent No. 6407063  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Duffour, Marie-Therese  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Cornelis, Guy  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Lurquin, Christophe  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: Chauv. Pascal  
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
; FILE REFERENCE: 11727  
; CURRENT APPLICATION NUMBER: US/09/165,863  
; CURRENT FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide  
US-09-165-863-22

Query Match 100.0%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

## RESULT 6

US-09-009-953-198 OK  
; Sequence 198, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly Reactive DR Restricted Epitopes  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,953  
; FILING DATE: 21-Jan-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,713  
; FILING DATE: 23-JAN-1997  
; APPLICATION NUMBER: US 60/037,432  
; FILING DATE: 07-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-011520US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 198:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 198:  
US-09-009-953-198

Query Match 100.0%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
DB 1 QNILLSNAPLGQFP 15

## RESULT 7

US-09-697-884-66  
Sequence 66, Application US/09697884  
Patent No. 6426217  
GENERAL INFORMATION:  
APPLICANT: Chauv, Pascal  
APPLICANT: Vantomme, Val,rie  
APPLICANT: Stroobant, Vincent  
APPLICANT: Boon-Falleur, Thierry  
APPLICANT: van der Bruggen, Pierre  
APPLICANT: Thielemans, Kris  
APPLICANT: Cortchal, Jurgen  
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
FILE REFERENCE: L0461/7052  
CURRENT APPLICATION NUMBER: US/09/697,884  
CURRENT FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: 09/166,448  
PRIOR FILING DATE: 1998-10-05  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 66  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-697-884-66

Query Match 100.0%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
DB 1 QNILLSNAPLGQFP 15

## RESULT 8

US-09-289-350-22  
Sequence 22, Application US/09289350  
Patent No. 6531451  
GENERAL INFORMATION:  
APPLICANT: Chauv, Pascal  
APPLICANT: Luiten, Rosalie  
APPLICANT: Demotte, Nathalie  
APPLICANT: Delfour, Marie-Therese  
APPLICANT: Lurquin, Christophe  
APPLICANT: Traversari, Catia  
APPLICANT: Stroobant, Vincent  
APPLICANT: Cornelis, Guy R.  
APPLICANT: Boon-Falleur, Thierry  
APPLICANT: Van Der Bruggen, Pierre  
TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
TITLE OF INVENTION: PROCEDURE  
FILE REFERENCE: 11727Z  
CURRENT APPLICATION NUMBER: US/09/289,350

CURRENT FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: 09/165,863  
PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 22  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Human Tyrosinase peptide  
US-09-289-350-22

Query Match 100.0%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
DB 1 QNILLSNAPLGQFP 15

## RESULT 9

US-09-574-749B-24  
Sequence 24, Application US/09574749B  
Patent No. 6548299  
GENERAL INFORMATION:  
APPLICANT: ROSENZWEIG, Michael  
APPLICANT: PYKETT, Mark J.  
APPLICANT: SCADDEN, David T.  
APPLICANT: POZNANSKY, Mark C.  
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
FILE REFERENCE: C1005/7012/KA/ERG  
CURRENT APPLICATION NUMBER: US/09/574,749B  
CURRENT FILING DATE: 2002-05-31  
PRIOR APPLICATION NUMBER: US 60/107,972  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: PCT/US99/26795  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 09/524,749  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 24  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Homo Sapiens source  
US-09-574-749B-24

Query Match 100.0%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
DB 1 QNILLSNAPLGQFP 15

## RESULT 10

US-09-318-141-22  
Sequence 22, Application US/09318141  
Patent No. 6602506  
GENERAL INFORMATION:  
APPLICANT: van der Bruggen, Pierre  
APPLICANT: Cornelis, Guy R.  
TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
TITLE OF INVENTION: WITH RECOMBINANT YERSINIA  
FILE REFERENCE: 11154  
CURRENT APPLICATION NUMBER: US/09/318,141  
CURRENT FILING DATE: 1999-05-25  
EARLIER APPLICATION NUMBER: US 09/036,582

```

? COUNTRY: USA
? ZIP: 14850
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/891,942G
? FILING DATE: 01-JUN-1992
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 06/915,753
? FILING DATE: 06-OCT-1986
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/362,847
? FILING DATE: 07-JUN-1989
? ATTORNEY/AGENT INFORMATION:
? NAME: Michaels, Christopher A
? REGISTRATION NUMBER: 34,390
? REFERENCE/DOCKET NUMBER: IND1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 607-273-1711
? TELEFAX: 607-273-2609
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 508 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-07-891-942G-10
?
? Query Match 100.0%; Score 79; DB 1;
? Best Local Similarity 100.0%; Pred. No. 2.7e-05;
? Matches 15; Conservative 0; Mismatches 0;
?
QY 1 QNILLSNAPLGQFPF 15
Db 56 QNILLSNAPLGQFPF 70
?
RESULT 13
US-07-891-942G-8
? Sequence 8, Application US/07891942G
? Patent No. 5679511
? GENERAL INFORMATION:
? APPLICANT: Kwon, Byoung Se
? TITLE OF INVENTION: CDNA CLONES FOR HUMAN TYROSIN
? TITLE OF INVENTION: A REGULATORY PROTEIN IN THE
? NUMBER OF SEQUENCES: 16
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Christopher A. Michaels, Barnard, B
? ADDRESSER: Michaels
? STREET: 306 East State Street; Suite 220
? CITY: Ithaca
? STATE: NY
? COUNTRY: USA
? ZIP: 14850
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/891,942G
? FILING DATE: 01-JUN-1992
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 06/915,753
? FILING DATE: 06-OCT-1986
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/362,847
? FILING DATE: 07-JUN-1989

```

ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A  
REGISTRATION NUMBER: 34,390  
REFERENCE/DOCKET NUMBER: IND1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 529 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-891-942G-8

Query Match 100.0%; Score 79; DB 1; Length 529;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
Db 56 QNILLSNAPLGQFP 70

RESULT 14  
US-08-370-909-19  
Sequence 19, Application US/08370909  
Patent No. 5843648  
GENERAL INFORMATION:  
APPLICANT: ROBBINS, PAUL F.; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: p15 AND TYROSINASE  
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC  
TITLE OF INVENTION: AND THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,909  
FILING DATE: 10-JAN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 529  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: PROTEIN  
US-08-370-909-19

Query Match 100.0%; Score 79; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15

Db 56 QNILLSNAPLGQFP 70

RESULT 15  
US-08-504-048-8  
Sequence 8, Application US/08504048  
Patent No. 5843674  
GENERAL INFORMATION:  
APPLICANT: TAKIMOTO, Hiroyuki  
APPLICANT: SUZUKI, Satoshi  
APPLICANT: SHIBATA, Koushi  
APPLICANT: MASUI, Shigeki  
TITLE OF INVENTION: ANTI-HUMAN TYROSINASE  
TITLE OF INVENTION: MONOCLONAL ANTIBODY  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/504,048  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: SATOT27.001APC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 529 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-504-048-8

Query Match 100.0%; Score 79; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
Db 56 QNILLSNAPLGQFP 70

RESULT 16  
US-09-341-982-1  
Sequence 1, Application US/09341982  
Patent No. 6558671  
GENERAL INFORMATION:  
APPLICANT: SLINGLUFF, Craig L.  
APPLICANT: HUNT, Donald F.  
APPLICANT: ENGELHARD, Victor H.

```
; APPLICANT: KITTLESEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; FILE REFERENCE: SLINGLOFF-3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-341-982-1

Query Match      100.0%; Score 79; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPP 15
Db 56 QNILLSNAPLGQPP 70

RESULT 17
US-09-169-717E-39
; Sequence 39, Application US/09169717E
; Patent No. 6667037
; GENERAL INFORMATION:
; APPLICANT: Ooms, Annie
; APPLICANT: DeGiovanni, Gerard
; APPLICANT: Morel, Sandra
; APPLICANT: Van den Eynde, Benoit
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolate Peptides Which Bind To HLA-B35 Molecules,
; TITLE OF INVENTION: Larger Peptides Which Contain These, Nucleic Acid
; TITLE OF INVENTION: Molecules Encoding Peptides, And Uses Thereof
; FILE REFERENCE: LUD561
; CURRENT APPLICATION NUMBER: US/09/169,717E
; CURRENT FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 39
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; US-09-169-717E-39

Query Match      100.0%; Score 79; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPP 15
Db 56 QNILLSNAPLGQPP 70

RESULT 18
US-10-011-436-4
; Sequence 4, Application US/10011436
; Patent No. 6669946
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Brichard, Vincent; Van Pel,
; Aline;
; Deplaen, Etienne; Coullie, Pierre; Renauld, Jean Christophe; Wolfel,
; Lethe, Bernard
; TITLE OF INVENTION: METHOD FOR IDENTIFYING INDIVIDUALS SUFFERING FROM
; CELLULAR ABNORMALITY SOME OF WHOSE ABNORMAL CELLS PRESENT C
; LEUCOCYTE
```

```
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 801 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.25inch, 1.44MB storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,436
; FILING DATE: 11-Dec-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/511,011
; FILING DATE: 5-AUGUST-1995
; APPLICATION NUMBER: 08/054,714
; FILING DATE: 28-APRIL-1993
; APPLICATION NUMBER: 07/994,928
; FILING DATE: 22-DECEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5299.9 DIV CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 662-0200
; TELEFAX: (202) 662-4643
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-011-436-4

Query Match      100.0%; Score 79; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQPP 15
Db 56 QNILLSNAPLGQPP 70

RESULT 19
US-08-540-922D-12
; Sequence 12, Application US/08540922D
; Patent No. 6284476
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Brichard, Vincent; Van
; APPLICANT: Pel, Aline; De Plaen, Etienne; Coullie, Pierre;
; APPLICANT: Renauld Jean-Christophe; Wolfel, Thomas; and
; APPLICANT: Lethe, Bernard
; TITLE OF INVENTION: METHOD OF IDENTIFYING INDIVIDUALS SUFFERING
; TITLE OF INVENTION: FROM A CELLULAR ABNORMALITY SOME OF WHOSE
; TITLE OF INVENTION: ABNORMAL CELLS PRESENT COMPLEXES OF HUMAN
; TITLE OF INVENTION: LEUCOCYTE ANTIGEN TYROSINASE DERIVED
; TITLE OF INVENTION: PEPTIDES, AND METHODS FOR TREATING SAID
; TITLE OF INVENTION: INDIVIDUALS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/540,922D  
FILING DATE: October 11, 1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,714  
FILING DATE: 28 April 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/994,928  
FILING DATE: 22 December 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mary Anne Schofield  
REGISTRATION NUMBER: 36,669  
REFERENCE/DOCKET NUMBER: LJD 5299.5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 537  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-540-922D-12

Query Match 100.0%; Score 79; DB 3; Length 537;  
Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
DB 64 QNILLSNAPLGQFP 78

## RESULT 20

US-07-891-942G-5  
Sequence 5, Application US/07891942G  
Patent No. 5679511  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung Se  
TITLE OF INVENTION: cDNA CLONES FOR HUMAN TYROSINASE AND FOR  
TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Christopher A. Michaels, Barnard, Brown &  
ADDRESSEE: Michaels  
STREET: 306 East State Street, Suite 220  
CITY: Ithaca  
STATE: NY  
COUNTRY: USA  
ZIP: 14850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/891,942G  
FILING DATE: 01-JUN-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/915,753  
FILING DATE: 06-OCT-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/362,847  
FILING DATE: 07-JUN-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A  
REGISTRATION NUMBER: 34,390

REFERENCE/DOCKET NUMBER: INDI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-891-942G-5

Query Match 100.0%; Score 79; DB 1; Length 560;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
DB 55 QNILLSNAPLGQFP 69

Search completed: June 3, 2004, 17:06:16  
Job time : 30 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:23:00 ; Search time 21 Seconds  
(without alignments)  
77.869 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_72

Perfect score: 90

Sequence: 1 QNILLSNAPLGPPFPPT 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2772

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	30.0	9	2 A61364	isotocin - common
2	27	30.0	16	2 PH1302	Ig heavy chain DJ
3	25	27.8	9	2 A91466	oxytocin - hippo
4	25	27.8	9	2 A92774	oxytocin - spotted
5	25	27.8	9	2 A93147	oxytocin - finback
6	25	27.8	9	2 A93408	oxytocin - Austral
7	25	27.8	9	2 B90667	oxytocin - rabbit
8	25	27.8	14	2 S33802	chaperone, TCPI-re
9	24	26.7	8	4 I54017	granulocyte-colony
10	24	26.7	9	2 A29477	diuretic neuropept
11	23.5	26.1	12	2 J00356	cycloleonorinin -
12	23	25.6	11	1 XAV1BH	bradykinin-potenti
13	23	25.6	12	2 S67528	napin - rape (frag
14	23	25.6	13	2 S09716	2S albumin large c
15	23	25.6	14	2 S23176	collagen alpha cha
16	23	25.6	14	2 PN0666	dystrophin-associa
17	23	25.6	15	2 B39109	hypothetical 1.5K
18	23	25.6	16	2 B41425	cytochrome P450 IF
19	22	24.4	13	1 XAV19B	angiotensin-conver
20	22	24.4	13	2 S33273	85K glycoprotein -
21	22	24.4	15	2 PN0144	serine proteinase
22	22	24.4	15	2 G61511	milk band B protei
23	22	24.4	16	1 A49761	locustapyrokinin -
24	22	24.4	16	2 D49655	T-cell-receptor be
25	21.5	23.9	12	2 PN0663	dystrophin-associa
26	21	23.3	8	2 PT0530	T-cell receptor be
27	21	23.3	9	2 D58503	translation elonga
28	21	23.3	9	2 S66635	alpha-2-macroglobu
29	21	23.3	11	2 C37196	bradykinin-potenti

30	21	23.3	11	2 D37196	bradykinin-potenti
31	21	23.3	11	2 PN0042	stathmin - mouse
32	21	23.3	12	2 PH1462	T-cell receptor be
33	21	23.3	13	2 D61491	seed protein ws-4
34	21	23.3	15	2 S27248	pseudogermin - whe
35	20.5	22.8	15	2 JN0730	hypothetical 1.7K
36	20	22.2	8	2 E47393	neuropeptide calla
37	20	22.2	8	2 A28719	thymic humoral fac
38	20	22.2	9	2 B28495	conpressin S - co
39	20	22.2	10	1 XASNPC	angiotensin-conver
40	20	22.2	10	2 A28953	alpha-conotoxin SI
41	20	22.2	13	2 S13273	polysialoglycoprot
42	20	22.2	14	2 B61309	lutropin beta chai
43	20	22.2	14	2 C48394	major fat-globule
44	20	22.2	15	2 B45115	peptidylprolyl iso
45	20	22.2	15	2 PN0665	dystrophin-associa

#### ALIGNMENTS

##### RESULT 1

A61364  
isotocin - common carp  
C;Species: Cyprinus carpio (common carp)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 20-Jun-2000  
C;Accession: A61364  
R;Acher, R.; Chauvet, J.; Chauvet, M.T.; Crepy, D.  
Comp. Biochem. Physiol. A 14, 245-254, 1965  
A;Title: Caractérisation des hormones neurohypophysaires d'un poisson osseux d'eau douce  
A;Reference number: A61364  
A;Accession: A61364  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <ACH>  
C;Superfamily: oxytocin-neurophysin  
C;Keywords: amidated carboxyl end; neuropeptide; posterior pituitary  
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.0%; Score 27; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 LSNAPLG 11  
DB 3 ISNCPIG 9

##### RESULT 2

PH1302  
IG heavy chain DJ region (clone C76-105) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: PH1302  
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma  
A;Reference number: PH1302; MUID:93094761; PMID:1460419  
A;Accession: PH1302  
A;Molecule type: DNA  
A;Residues: 1-16 <WAS>  
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 27; DB 2; Length 16;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 PLGPQFP 15  
DB 10 PLGPFPNP 16

##### RESULT 3



A91466  
oxytocin - hippopotamus  
N;Alternate names: neurophysin I  
N;Contains: neurophysin 1; oxytocin  
C;Species: Hippopotamus amphibius (hippopotamus)  
C;Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C;Accession: A91466; A01450; B01450  
R;Ferguson, D.R.; Pickering, B.T.  
Gen. Comp. Endocrinol. 13, 425-429, 1969  
A;Title: Arginine and lysine vasopressins in the hippopotamus neurohypophysis.  
A;Reference number: A91466; MUID:71232719; PMID:5406007  
A;Accession: A91466  
A;Molecule type: protein  
A;Residues: 1-9 <FER>  
C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
C;Superfamily: oxytocin-neurophysin  
C;Keywords: amidated carboxyl end; hormone; hypothalamus  
F;1-6/Disulfide bonds: #status predicted  
F;9/Modified site: amidated carboxyl end (Gly) #status predicted

Query Match 27.8%; Score 25; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLG 11  
: |||||  
Db 3 IQNCPLG 9

RESULT 4  
A92774  
oxytocin - spotted ratfish  
N;Alternate names: neurophysin I  
N;Contains: neurophysin 1; oxytocin  
C;Species: Hydrolagus collii (spotted ratfish)  
C;Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C;Accession: A92774; A01450; B01450  
R;Pickering, B.T.; Heller, H.  
J. Endocrinol. 45, 597-606, 1969  
A;Title: Oxytocin as a neurohypophysial hormone in the holoccephalian elasmobranch fish.  
A;Reference number: A92774; MUID:70088110; PMID:5365118  
A;Accession: A92774  
A;Molecule type: protein  
A;Residues: 1-9 <PIC>  
C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
C;Superfamily: oxytocin-neurophysin  
C;Keywords: amidated carboxyl end; hormone; hypothalamus  
F;1-6/Disulfide bonds: #status predicted  
F;9/Modified site: amidated carboxyl end (Gly) #status predicted

Query Match 27.8%; Score 25; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLG 11  
: |||||  
Db 3 IQNCPLG 9

RESULT 5  
A93147  
oxytocin - finback whale  
N;Alternate names: neurophysin I  
N;Contains: neurophysin 1; oxytocin  
C;Species: Balaeoptera physalus (finback whale, common rorqual)  
C;Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C;Accession: A93147; A01450; B01450  
R;Acher, R.; Chauvet, J.; Chauvet, M.T.  
Nature 201, 191-192, 1964  
A;Title: Isolation of finback whale oxytocin and vasopressin.  
A;Reference number: A93147  
A;Accession: A93147  
A;Molecule type: protein

Query Match 27.8%; Score 25; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLG 11  
: |||||  
Db 3 IQNCPLG 9

A;Residues: 1-9 <ACH>  
C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
C;Superfamily: oxytocin-neurophysin  
C;Keywords: amidated carboxyl end; hormone; hypothalamus  
F;1-6/Disulfide bonds: #status experimental  
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 27.8%; Score 25; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLG 11  
: |||||  
Db 3 IQNCPLG 9

RESULT 6  
A93408  
oxytocin - Australian echidna  
N;Alternate names: neurophysin I  
N;Contains: neurophysin 1; oxytocin  
C;Species: Tachyglossus aculeatus (Australian echidna)  
C;Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C;Accession: A93408; A01450; B01450  
R;Acher, R.; Chauvet, J.; Chauvet, M.T.  
Nature New Biol. 244, 124-126, 1973  
A;Title: Neurohypophysial hormones and evolution of tetrapods.  
A;Reference number: A93408; MUID:73223515; PMID:4515919  
A;Accession: A93408  
A;Molecule type: protein  
A;Residues: 1-9 <ACH>  
C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
C;Superfamily: oxytocin-neurophysin  
C;Keywords: amidated carboxyl end; hormone; hypothalamus  
F;1-6/Disulfide bonds: #status predicted  
F;9/Modified site: amidated carboxyl end (Gly) #status predicted

Query Match 27.8%; Score 25; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLG 11  
: |||||  
Db 3 IQNCPLG 9

RESULT 7  
B90667  
oxytocin - rabbit  
N;Alternate names: neurophysin I  
N;Contains: neurophysin 1; oxytocin  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C;Accession: B90667; A01450; B01450  
R;Chauvet, J.; Chauvet, M.T.; Acher, R.  
Biochimie 53, 1099-1104, 1971  
A;Title: Evolution des hormones neurohypophysaires: isolement des principes actifs du la  
A;Reference number: A90667; MUID:72215060; PMID:5150741  
A;Accession: B90667  
A;Molecule type: protein  
A;Residues: 1-9 <CHA>  
C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
C;Superfamily: oxytocin-neurophysin  
C;Keywords: amidated carboxyl end; hormone; hypothalamus  
F;1-6/Disulfide bonds: #status experimental  
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 27.8%; Score 25; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLG 11  
: |||||

Db 3 IQNCPLG 9

## RESULT 8

S33802  
C:Species: avena sativa (oat)  
C:Date: 02-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 17-Mar-1999  
C:Accession: S33802  
R:Mummert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaefer  
Nature 363, 644-648, 1993  
A:Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its photo  
A:Reference number: S33800; MUID:93288140; PMID:8099715  
A:Accession: S33802  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <MUM>

Query Match 27.8%; Score 25; DB 2; Length 14;  
Best Local Similarity 62.5%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLGP 12

Db 2 LESAKLGP 9

## RESULT 9

I54017  
granulocyte-colony stimulating factor precursor - synthetic (fragment)  
C:Species: synthetic  
A:Note: human gene engineered and expressed in *Escherichia coli*  
C:Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000  
C:Accession: I54017  
R:Devlin, P.E.; Drummond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.  
Gene 65, 13-22, 1988  
A:Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac  
1.  
A:Reference number: I54017; MUID:88284374; PMID:2456256  
A:Accession: I54017  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-8 <DEV>  
A:Cross-references: GB:M20922; NID:9806638; PIDN:AAA66353.1; PID:gl83043

Query Match 26.7%; Score 24; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLGP 12

Db 3 PLGP 6

## RESULT 10

A29477  
diuretic neuropeptide F1 - migratory locust  
C:Species: Locusta migratoria (migratory locust)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 31-Dec-1993  
C:Accession: A29477  
R:Proulx, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delaage, M.; Schooley  
Biochem. Biophys. Res. Commun. 149, 180-186, 1987  
A:Title: Identification of an arginine vasopressin-like diuretic hormone from *Locusta mi*  
A:Reference number: A29477; MUID:88077077; PMID:3689410  
A:Accession: A29477  
A:Molecule type: protein  
A:Residues: 1-9 <PRO>  
A:Note: two neuropeptides, F1 and F2, were identified. F2 is an antiparallel dimer of F1  
C:Keywords: neuropeptide

Query Match 26.7%; Score 24; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LLSNAPLG 11

Db 2 LITNCPG 9

## RESULT 11

JU0356  
cycloleonorinin - sagebrush motherwort  
C:Species: Leonurus artemisia (sagebrush motherwort)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: JU0356  
R:Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.  
Chem. Pharm. Bull. 39, 712-715, 1991  
A:Title: Cycloleonorinin, a cyclic peptide from *Leonuri fructus*.  
A:Reference number: JU0356; MUID:91300597; PMID:2070452  
A:Accession: JU0356  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <KIN>

Query Match 26.1%; Score 23.5; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 6.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 9 PLGP-QFP 15

Db 3 PAGPTQYP 10

## RESULT 12

XAVIBH  
bradykinin-potentiating peptide - halys viper  
N:Alternate names: BPP  
C:Species: Agkistrodon halys (halys viper)  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 05-Aug-1994  
C:Accession: JCO002  
R:Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.  
Peptides 6, 339-342, 1985  
A:Title: Structure-function studies on the bradykinin potentiating peptide from Chinese  
A:Reference number: JCO002; MUID:86177022; PMID:3008123  
A:Accession: JCO002  
A:Molecule type: protein  
A:Residues: 1-11 <CHI>  
C:Comment: Because this peptide both inhibits the activity of the angiotensin-converting  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyro  
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.6%; Score 23; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 PLGPQFP 15

Db 4 PPGPPIP 10

## RESULT 13

S67528  
napin - rape (fragments)  
C:Species: Brassica napus (rape)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S67528  
R:Muren, E.; Ek, B.; Rask, L.  
Eur. J. Biochem. 227, 316-321, 1995  
A:Title: Processing of the 2S storage protein pronapin in *Brassica napus* and in transfor  
A:Reference number: S67528; MUID:95154306; PMID:7851402  
A:Accession: S67528  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6;7-12 <MUR>

Query Match 25.6%; Score 23; DB 2; Length 12;  
Best Local Similarity 80.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PLGFPQ 13  
|  
|  
|  
|  
Db 7 PQGFPQ 11

## RESULT 14

S09716  
2S albumin large chain (1 and 2) nII - rape (fragments)  
N;Alternate names: 2S albumin large chain nIII  
C;Species: Brassica napus (rape)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Aug-1998  
C;Accession: S09716; S09718; S09717  
R;Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.  
FEBS Lett. 263, 209-212, 1990  
A;Title: beta-turns as structural motifs for the proteolytic processing of seed proteins  
A;Reference number: S09720; MUID:90242974; PMID:2185951  
A;Accession: S09716  
A;Molecule type: protein  
A;Residues: 1-9;10-13 <MON>  
A;Experimental source: seed  
A;Note: 3-Ser was also found  
A;Accession: S09718  
A;Molecule type: protein  
A;Residues: 1-9;10-13 <MO2>  
A;Experimental source: seed  
A;Accession: S09717  
A;Molecule type: protein  
A;Residues: 1-9;10-13 <MO3>  
A;Experimental source: seed

Query Match 25.6%; Score 23; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PLGFPQ 13  
|  
|  
|  
|  
Db 1 PQGFPQ 5

## RESULT 15

S23376  
collagen alpha chain - polychaete (Alvinella pompejana) (fragment)  
C;Species: Alvinella pompejana  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 29-May-1998  
C;Accession: S23376  
R;Gall, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J.  
J. Mol. Biol. 221, 209-223, 1991  
A;Title: Molecular characterization of cuticle and interstitial collagens from worms col  
A;Reference number: S17581; MUID:92015209; PMID:1920405  
A;Accession: S23376  
A;Molecule type: protein  
A;Residues: 1-14 <GAI>

Query Match 25.6%; Score 23; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 8.9e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLGFPQ 13  
|  
|  
|  
|  
Db 7 PMGPR 11

Search completed: June 3, 2004, 15:27:17  
Job time : 22 secs

RESULT 2	ISOT_CYPCA	STANDARD;	PRT;	9 AA.
ID	ISOT_CYPCA			
AC	P42953;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Isotocin.			
OS	Cyprinus carpio (Common carp) .			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Cyprinus.			
OX	NCBI_TaxID=7962;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Pituitary;			
RA	Acher R., Chauvet J., Chauvet M.-T., Crepy D.;			

```

RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes."
RL Comp. Biochem. Physiol. 14:245-254 (1965).
CC -1- FUNCTION: ANTIDIURETIC HORMONE.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; A61364; A61364.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match
Best Local Similarity 30.0%; Score 27; DB 1; Length 9;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 LSNAPLG 11
DB 3 ISNCPG 9

RESULT 3
OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42939;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophyseal hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias."
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; 17FB376EB444404B CRC64;

Query Match
Best Local Similarity 28.9%; Score 26; DB 1; Length 9;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 LSNAPLG 11
DB 3 INNCPLUG 9

RESULT 4
OXYT_RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;

```

```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit),
OS Hippopotamus amphibius (Hippopotamus), (Common torqual),
OS Balanoptera physalus (Finback whale),
OS Tachyotus aculeatus aculeatus (Australian echidna), and
OS Hydrolagus collei (Spotted ratfish) (Pacific ratfish),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats."
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RX SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RL neurohypophysis."
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RX SPECIES=B. physalus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin."
RL Nature 201:191-192(1964).
RN [4]
RP SEQUENCE.
RX SPECIES=A. aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophyseal hormones and evolution of tetrapods."
RL Nature New Biol. 244:124-126(1973).
RN [5]
RP SEQUENCE.
RX SPECIES=H. collei;
RX MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophyseal hormone in the holoccephalian
RT elasmobranch fish, Hydrolagus collei."
RL J. Endocrinol. 45:597-606(1969).
CC -1- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; A91466; A91466.
DR PIR; A92774; A92774.
DR PIR; A93147; A93147.
DR PIR; A93408; A93408.
DR PIR; B90667; B90667.
DR PDB; 1XY1; 15-OCT-90.
DR PDB; 1XY2; 15-OCT-90.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1010 MW; 17FB376EB456D04B CRC64;

Query Match
Best Local Similarity 27.8%; Score 25; DB 1; Length 9;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLG 11
DB 3 INNCPLUG 9

```

Db 3 IONCPLG 9

RESULT 5  
DNFI LOCFI  
ID DNFI LOCFI STANDARD; PRT; 9 AA.  
AC F16339;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Locupressin (Diuretic neuropeptide F1/F2).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Subesophageal ganglion, and Thoracic ganglion;  
RX MEDLINE=88077077; PubMed=3689410;  
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,  
RA Delaage M., Schooley D.A.;  
RT "Identification of an arginine vasopressin-like diuretic hormone from  
RT Locusta migratoria.";  
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).  
CC -!- FUNCTION: DIURETIC HORMONE.  
CC -!- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.  
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.  
DR PIR; A29477; A29477.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Neuropeptide; Amidation.  
FT DISULFID 1 6 IN F1.  
FT DISULFID 1 1 INTERCHAIN (WITH C-6) (IN F2).  
FT DISULFID 1 6 INTERCHAIN (WITH C-1) (IN F2).  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 26.7%; Score 24; DB 1; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LLSNAPLG 11  
|::|||  
Db 2 LITNCPRG 9

RESULT 6  
OXYA SCYCA  
ID OXYA SCYCA STANDARD; PRT; 9 AA.  
AC P42996;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Asvatocin.  
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
OC Scyliorhinidae; Scyliorhinus.  
NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.  
RC TISSUE= Pituitary;  
RX MEDLINE=95062247; PubMed=7972045;  
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;  
RT "Special evolution of neurohypophysial hormones in cartilaginous  
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides  
RT isolated from the spotted dogfish (Scyliorhinus canicula).";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).  
CC -!- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.  
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.  
DR InterPro; IPR000981; Neurhyp\_horm.

DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 25.6%; Score 23; DB 1; Length 9;  
Best Local Similarity 42.9%; Pred. No. 1.4e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 LSNAPLG 11  
|::|||  
Db 3 INNCPVG 9

RESULT 7  
OXYT RAJCL  
ID OXYT RAJCL STANDARD; PRT; 9 AA.  
AC P42994;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Glutitocin.  
OS Raja clavata (Thornback ray).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squalia; Hymnosqualea; Pristiogoralea; Batoidea;  
OC Rajiformes; Rajidae; Raja.  
NCBI\_TaxID=7781;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=66123415; PubMed=5880565;  
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
RT "Phylogeny of neurohypophysial peptides: isolation of a new hormone,  
RT glutitocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,  
RT the ray (Raja clavata).";  
RL Biochim. Biophys. Acta 107:393-396(1965).  
CC -!- FUNCTION: ANTIDIURETIC HORMONE.  
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 984 MW; 17B9C76EB45B04B CRC64;

Query Match 25.6%; Score 23; DB 1; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.4e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLG 11  
|::|||  
Db 3 INNCPVG 9

RESULT 8  
BPP AGKHP  
ID BPP AGKHP STANDARD; PRT; 11 AA.  
AC P04562;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys pallasi (Chinese water moccasin) (Gloydus halys  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidogauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydus.  
NCBI\_TaxID=8714;  
RN [1]  
RP SEQUENCE.

```

RC TISSUE=Venom;
RA MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RL from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BAF1277686777 CRC64;

Query Match 25.6%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 PLGQPP 15
DB 4 PGQPP 10

RESULT 9
CYSK_CLOPA STANDARD; PRT; 15 AA.
AC P81340;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cysteine synthase (EC 2.5.1.47) (O-acetylserine sulphydrylase) (O-
DE acetylserine (thiol)-lyase) (CSase) (CP 27) (Fragment).
GN CYSK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- CATALYTIC ACTIVITY: O(3)-acetyl-L-serine + H(2)S = L-cysteine +
CC acetate.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: Cysteine biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the cysteine synthase/cystathionine beta-
CC synthase family.
DR InterPro; IPR001216; Cys synthase BS.
DR PROSITE; PS00901; CYS SYNTHASE; PARTIAL.
KW Transferase; Cysteine biosynthesis; Pyridoxal phosphate.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1625 MW; 0196582B9671A352 CRC64;

Query Match 25.6%; Score 23; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LLSNAPL 10
DB 5 LIGNTPL 11

RESULT 10
OXYV_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)

```

```

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squalidae; Squaloidei; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match 24.4%; Score 22; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LSNAPLG 11
DB 3 IQNCPVG 9

RESULT 11
UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Plasma;
RX MEDLINE=9302937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.5, its MW is: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 24.4%; Score 22; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 PQFPPT 17

```

```

Db          1 1 1 1
2 PLFEXT 7

RESULT 12
ID BPPI BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3,1 (13A) (Angiotensin-converting
DE enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724, 8723;
RN [1]
RN [2]
RP SEQUENCE.
RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01253; XAVI9B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match 24.4%; Score 22; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 7.9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPOPF 15
DB 8 GPEIP 12

RESULT 13
ID SODM ENTAE STANDARD; PRT; 15 AA.
AC P22799;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
GN SODA.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RN [2]
RP SEQUENCE.
RX MEDLINE=91248479; PubMed=1368658;
RA Kim S.W., Lee S.O., Lee T.H.;
RT "Purification and characterization of superoxide dismutase from
RT Aerobacter aerogenes.";

```

```

Agric. Biol. Chem. 55:101-108(1991).
-1- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
-1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
-1- SUBUNIT: Homodimer.
-1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
DR PIR; PNO615; PNO615.
DR InterPro; IPR001189; SODismutase.
PFam; PF00081; sodfe; 1.
DR PROSITE; PS00086; SOD_MN; PARTIAL.
KW Oxidoreductase; Metal-binding; Iron.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1756 MW; 352F3D949202B642 CRC64;

Query Match 24.4%; Score 22; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 PQPPF 16
DB 5 PQLPY 9

RESULT 14
ID LPK1 LOCFM STANDARD; PRT; 16 AA.
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 1 (LOM-PK-1).
OS Locusta migratoria 1 (LOM-PK-1).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RN [2]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=91224474; PubMed=2026322;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
RT myotropic peptide of Locusta migratoria.";
RL Gen. Comp. Endocrinol. 81:97-104(1991).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SIMILARITY: Belongs to the pyrokinin family.
DR PIR; A49761; A49761.
DR InterPro; IPR001484; PYROKININ.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;

Query Match 24.4%; Score 22; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 PQPPF 16
DB 8 PQPPF 12

RESULT 15
ID OXYF SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

```



```

DE Phasvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chordrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7930;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB4449DB CRC64;
AMIDATION.
Query Match 23.3%; Score 21; DB 1; Length 9;
Best Local Similarity 50.0%; Pred.No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 6 SNAPLG 11
Db 4 NNCFVG 9

```

Search completed: June 3, 2004, 15:25:51  
Job time : 11 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:22:20 ; Search time 39 Seconds  
(without alignments)  
137.534 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_72

Perfect score: 90

Sequence: 1 QNLLSNAPLGQPPPT 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 4499

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	30.0	16	4 Q8NHY1	Q8nhy1 homo sapien
2	26	28.9	15	6 Q9TRN8	Q9trn8 sus scrofa
3	25	27.8	11	2 Q48933	Q48933 mycobacteri
4	25	27.8	12	6 P83127	P83127 bos indicus
5	25	27.8	16	6 O77489	O77489 tupaiia glis
6	24	26.7	11	2 O87882	O87882 mycobacteri
7	24	26.7	13	10 Q43174	Q43174 solanum tub
8	24	26.7	15	6 Q9TR03	Q9tr03 bos taurus
9	24	26.7	16	5 Q9TWK1	Q9twk1 mytilus edu
10	23	25.6	16	5 Q9TWK0	Q9twk0 mytilus edu
11	22	24.4	10	10 P82438	P82438 nicotiana t
12	22	24.4	14	2 P81715	P81715 streptomyce
13	22	24.4	15	6 Q9TRN7	Q9trn7 sus scrofa
14	22	24.4	16	10 Q8RVF4	Q8rvf4 zea mays (m
15	21	23.3	7	3 P83492	P83492 bionectria
16	21	23.3	11	12 Q80GPO	Q80gpo tomato leaf

```

17 21 23.3 12 2 Q8KZ86
18 21 23.3 12 8 Q85G95
19 21 23.3 14 2 P81801
20 21 23.3 14 8 Q85G97
21 21 23.3 14 8 Q85G92
22 21 23.3 16 2 Q51436
23 20.5 22.8 11 12 Q80B26
24 20.5 22.8 12 6 Q8MJQ0
25 20.5 22.8 12 6 Q8MJP8
26 20.5 22.8 12 6 Q8MJP7
27 20.5 22.8 12 6 Q8MJP9
28 20.5 22.8 12 6 Q8MJQ1
29 20.5 22.8 12 6 Q8MJQ1
30 20.5 22.8 12 6 Q8MJE2
31 20 22.2 7 15 Q07624
32 20 22.2 10 13 Q90Y93
33 20 22.2 13 12 P90442
34 20 22.2 14 2 Q9R517
35 20 22.2 14 11 Q70599
36 20 22.2 14 15 Q8JDM3
37 20 22.2 14 15 Q8JDM7
38 20 22.2 14 15 Q8JDM0
39 20 22.2 15 12 Q69353
40 20 22.2 16 11 Q54894
41 20 22.2 16 11 Q9JHM3
42 20 22.2 16 11 Q9QZY3
43 19.5 21.7 16 6 Q9TR99
44 19.5 21.7 16 8 Q8HU42
45 19.5 21.7 16 8 Q8HU29

```

#### ALIGNMENTS

#### RESULT 1

```

Q8NHY1
ID Q8NHY1 PRELIMINARY; PRT; 16 AA.
AC Q8NHY1;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hepatic nuclear factor 4 alpha (fragment).
GN HNF4A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21592951; PubMed=11717395;
RA Boj S.F., Parrizas M., Maestro M.A., Ferrer J.;
RT "A transcription factor regulatory circuit in differentiated
RT pancreatic cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:14481-14486(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Boj S.F., Parrizas M., Ferrer J.;
RT "HNF4A expression in human pancreatic cells.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF509467; AAM34296.2; -.
FT NON TER 16
SQ SEQUENCE 16 AA; 1621 MW; 1F4CE5E2B61FF009 CRC64;

```

Query Match 30.0%; Score 27; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NAPLG 11

Db 5 NAPLG 9

#### RESULT 2

## Q9TRN8

ID Q9TRN8 PRELIMINARY; PRT; 15 AA.  
 AC Q9TRN8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 67 kDa zona pellucida binding protein homolog (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 ON NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92378926; PubMed=1510840;  
 RA Parry R.V., Barker P.J., Jones R.;  
 RT "Characterization of low Mr zona pellucida binding proteins from boar  
 spermatozoa and seminal plasma";  
 RL Mol. Reprod. Dev. 33:108-115(1992).  
 SQ SEQUENCE 15 AA; 1593 MW; 176B80F981EF1858 CRC64;

Query Match 28.9%; Score 26; DB 6; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GQGFPT 17  
 DB 5 GPLIPT 11

## RESULT 3

ID Q48933 PRELIMINARY; PRT; 11 AA.  
 AC Q48933; P77701; Q48932;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DE Alkyl hydroperoxide reductase C (Fragment).  
 GN AHPC.  
 OS Mycobacterium bovis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 ON NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC35728, and ATCC35727;  
 RA Zhang Y., Deretic V.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC35735;  
 RX MEDLINE=96256622; PubMed=8655566;  
 RA Dhandayathapani S., Zhang Y., Deretic V.;  
 RT "Oxidative stress response and its role in sensitivity to isoniazid in  
 Mycobacterium smegmatis and inducibility of ahpc by peroxides in  
 Mycobacterium tuberculosis";  
 RT J. Bacteriol. 178:3641-3649(1996).  
 RL EMBL; U58031; AAB00320.1; -;  
 DR EMBL; U57979; AAA99830.1; -;  
 DR EMBL; U57978; AAA99829.1; -;  
 DR EMBL; U57762; AAB00317.1; -;  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1231 MW; 455099E3A87041A7 CRC64;

Query Match 27.8%; Score 25; DB 2; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 LGQFPF 15  
 DB 6 IGDQFP 11

## RESULT 4

ID P83127 PRELIMINARY; PRT; 12 AA.  
 AC P83127;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Alpha-N-acetylgalactosaminidase (EC 3.2.1.49) (Fragment).  
 OS Bos indicus (Zebu).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 ON NCBI\_TaxID=9915;  
 RN [1]  
 RP SEQUENCE, AND GLYCOSYLATION.  
 RC TISSUE=Placenta;  
 RA Sousa N.M., Remy B., El Amiri B., Figueiredo J.R., Beckers J.F.;  
 RT "Characterization of pregnancy-associated glycoproteins extracted from  
 zebu (Bos indicus) placentas removed at different gestational  
 periods";  
 RL Submitted (OCT-2001) to Swiss-Prot.  
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING N-  
 ACETYL-D-GALACTOSAMINE RESIDUES IN N-ACETYL-ALPHA-D-  
 GALACTOSAMINIDES.  
 CC -!- SUBCELLULAR LOCATION: LYSOSOMAL (BY SIMILARITY).  
 CC -!- PTM: GLYCOSYLATED.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 27 OF GLYCOSYL HYDROLASES.  
 DR GO; GO:0005764; C:lysosome; IEA.  
 DR GO; GO:0008456; F:alpha-N-acetylgalactosaminidase activity; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR000111; Glyco hydro GHD.  
 DR PROSITE; PS00512; ALPHA-GALACTOSIDASE; PARTIAL.  
 KW Hydrolase; Glycosidase; Glycoprotein; Lysosome.  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1325 MW; 53B124381F240727 CRC64;

Query Match 27.8%; Score 25; DB 6; Length 12;  
 Best Local Similarity 45.5%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QNILLSNAPLG 11  
 DB 2 ENGLRKPPMG 12

## RESULT 5

ID O77489 PRELIMINARY; PRT; 16 AA.  
 AC O77489;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE D4 dopamine receptor (D4Dr) (Fragment).  
 OS Tupia glis (Tree shrew).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.  
 ON NCBI\_TaxID=9395;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Inoue-Murayama M., Takenaka O., Murayama Y.;  
 RT "Origin and divergence of tandem repeats of primate D4 dopamine  
 receptor genes";  
 RL Primates 39:217-224(1998).  
 DR EMBL; AB016198; BAA32036.1; -;  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1577 MW; 3865AEE77FB63E09 CRC64;

Query Match 27.8%; Score 25; DB 6; Length 16;  
 Best Local Similarity 62.5%; Pred. No. 2.1e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 PLGPQPPF 16  
| | | | |  
Db 3 PGSPQDPF 10

RESULT 6  
O87882 ID O87882 PRELIMINARY; PRT; 11 AA.  
AC O87882;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Alkyl hydroperoxide reductase (Fragment).  
GN AHPC.  
OS Mycobacterium xenopi.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1789;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC19250;  
RX MEDLINE=98406038; PubMed=9733688;  
RA Pagan-Ramos E., Song J., McFalone M., Mudd M.H., Deretic V.;  
RT "Oxidative stress response and characterization of the oxyR-ahpc and  
RT furA-katG loci in Mycobacterium marinum";  
RL J. Bacteriol. 180:4856-4864(1998).  
DR ENBL; U43810; AAC61663.1; -;  
FT NON TER 11  
SQ SEQUENCE 11 AA; 1147 MW; 45458CE1787041A7 CRC64;

Query Match 26.7%; Score 24; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 LGPQPP 15  
: | | | |  
Db 6 IGGQFP 11

RESULT 7  
Q43174 ID Q43174 PRELIMINARY; PRT; 13 AA.  
AC Q43174;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Beta-fructofuranosidase (EC 3.2.1.26) (Fragment).  
OS Solanum tuberosum (Potato)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Cara;  
RX MEDLINE=96279736; PubMed=8710506;  
RA Bournay A.S., Hedley P.E., Maddison A., Waugh R., Machray G.C.;  
RT "Exon skipping induced by cold stress in a potato invertase gene  
RT transcript";  
RL Nucleic Acids Res. 24:2347-2351(1996).  
DR EMBL; X5821; CAA5087.1; -;  
DR GO; GO:0004564; F-beta-fructofuranosidase activity; IEA.  
DR GO; GO:0016798; F-hydrolase activity, acting on glycosyl bonds; IEA.  
DR GO; GO:0005975; P-carbohydrate metabolism; IEA.  
KW Glycosidase; Hydrolase.  
FT NON TER 1  
FT NON TER 13  
SQ SEQUENCE 13 AA; 1541 MW; 1B3053E7384C6874 CRC64;

Query Match 26.7%; Score 24; DB 10; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.5e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 NAPLGPQF 14  
| | | | |  
Db 3 NDENGPMY 10

RESULT 8  
Q9TR03 ID Q9TR03 PRELIMINARY; PRT; 15 AA.  
AC Q9TR03;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE Neuron-specific ASH/GRB-2 SH3 domain-binding protein (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96257761; PubMed=8687411;  
RA Miura K., Miki H., Shimazaki K., Kawai N., Takenawa T.;  
RT "Interaction of Ash/Grb-2 via its SH3 domains with neuron-specific  
RT p150 and p65";  
RL Biochem. J. 316:639-645(1996).  
SQ SEQUENCE 15 AA; 1635 MW; 25161E83C374F9CD CRC64;

Query Match 26.7%; Score 24; DB 6; Length 15;  
Best Local Similarity 57.1%; Pred. No. 2.9e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 PLGPQPP 15  
| | | | |  
Db 5 PNGPNLP 11

RESULT 9  
Q9TWK1 ID Q9TWK1 PRELIMINARY; PRT; 16 AA.  
AC Q9TWK1;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE Proximal collagen (Fragment).  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
OC Mytiloidea; Mytilidae; Mytilus.  
OX NCBI\_TaxID=6550;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95230211; PubMed=7714453;  
RA Qin X., Waite J.H.;  
RT "Exotic collagen gradients in the byssus of the mussel Mytilus  
RT edulis";  
RL J. Exp. Biol. 198:633-644(1995).  
SQ SEQUENCE 16 AA; 1418 MW; 72887820BC382660 CRC64;

Query Match 26.7%; Score 24; DB 5; Length 16;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PLGPQ 13  
| | | | |  
Db 3 PAGPQ 7

RESULT 10  
Q9TWK0 ID Q9TWK0 PRELIMINARY; PRT; 16 AA.  
AC Q9TWK0;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Proximal collagen (Fragment)  
 OS Mytilus edulis (Blue mussel)  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;  
 OC Mytiloidae; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RN SEQUENCE.

RP MEDLINE=95230211; PubMed=7714453;  
 RA Qin X., Waite J.H.;  
 RT "Exotic collagen gradients in the byssus of the mussel Mytilus  
 edulis.";  
 RL J. Exp. Biol. 198;633-644(1995).  
 SQ SEQUENCE 16 AA; 1347 MW; B57F18783A18783C CRC64;

Query Match 25.6%; Score 23; DB 5; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 4.6e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PLGPQ 13  
 |||||  
 Db 2 PQGPQ 6

## RESULT 11

P82438 ID P82438 PRELIMINARY; PRT; 10 AA.  
 AC P82438;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 24, Last annotation update)  
 DE 50 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RN SEQUENCE.

RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 tobacco culture."  
 RL Planta 0:0-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1126 MW; C68E32486AF77B46 CRC64;

Query Match 24.4%; Score 22; DB 10; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 4.2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 PQPP 15  
 |||||  
 Db 2 PQYP 5

## RESULT 12

P81715 ID P81715 PRELIMINARY; PRT; 14 AA.  
 AC P81715;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DE LeuPTin-inactivating enzyme (EC 3.4.24.-) (LIE) (Fragment).  
 OS Streptomyces exfoliatus (Streptomyces hydrogenans).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI\_TaxID=1905;  
 RN [1]  
 RN SEQUENCE.  
 RC STRAIN=SMF13;  
 RX PubMed=9531495;  
 RA Kim I.S., Kim Y.B., Lee K.J.;  
 RT "Characterization of the leuPTin-inactivating enzyme from  
 Streptomyces exfoliatus SMF13 which produces leuPTin.";  
 RL Biochem. J. 331:539-545(1998).  
 CC -1- FUNCTION: A LEUCINE-SPECIFIC METALLOPROTEASE THAT PLAYS A ROLE IN  
 CONTROLLING THE AMOUNT OF LEUPEPTIN DURING COLONY DEVELOPMENT.  
 CC OPTIMUM PH IS 9.0 AND TEMPERATURE IS 40 DEGREES CELSIUS.  
 CC -1- FUNCTION: DEGRADES LEUPEPTIN INTO THREE COMPONENTS, ACETYL-  
 LEUCINE, LEUCINE AND ARGININAL.  
 CC -1- CATALYTIC ACTIVITY: HAS A STRICT PREFERENCE FOR LEUCINE AT THE P1  
 SITE.  
 CC -1- ENZYME REGULATION: ACTIVITY IS INHIBITED BY METALLOPROTEASE  
 INHIBITORS AND ACTIVATED BY MG2+ AND CA2+.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: SECRETED  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0008237; F:metalloprotease activity; IEA.  
 KW Hydrolase; Metalloprotease.  
 FT NON TER 14 14  
 SQ SEQUENCE 14 AA; 1373 MW; 14D627940C973260 CRC64;

Query Match 24.4%; Score 22; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 6e+03;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 APLGPQFP 15  
 |||||  
 Db 1 APTPPDIP 8

## RESULT 13

Q9TRN7 ID Q9TRN7 PRELIMINARY; PRT; 15 AA.  
 AC Q9TRN7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 72 kDa zona pellucida binding protein homolog (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RN SEQUENCE.

RX MEDLINE=92378826; PubMed=1510840;  
 RA Parry R.V., Barker P.J., Jones R.;  
 RT "Characterization of low Mr zona pellucida binding proteins from boar  
 spermatozoa and seminal plasma.";  
 RL Mol. Reprod. Dev. 33:108-115(1992).  
 SQ SEQUENCE 15 AA; 1574 MW; 09C9A1C686F386F8 CRC64;

Query Match 24.4%; Score 22; DB 6; Length 15;  
 Best Local Similarity 54.5%; Pred. No. 6.5e+03;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NILLSNAPLGP 12  
 |||||  
 Db 4 NIVLIFALLSP 14

## RESULT 14

Q8RVF4 ID Q8RVF4 PRELIMINARY; PRT; 16 AA.  
 AC Q8RVF4;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Proline rich protein (Fragment).

```

OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=cv. H98, and cv. C123;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094252; AA015707.1; -.
DR EMBL; AY094253; AA015708.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1720 MW; 02F6CD77295B5610 CRC64;

Query Match 24.4%; Score 22; DB 10; Length 16;
Best Local Similarity 55.8%; Pred. No. 7e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 NAPLGPQFP 15
Db 4 HAPSGEQCP 12

RESULT 15
P83492
ID P83492 PRELIMINARY; PRT; 7 AA.
AC P83492;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).
OS Bionectria ochroleuca (Glocladium roseum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.
OX NCBI_TaxID=29856;
RN [1]_
RP SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=Gr87;
RA Zhao M., Zhang K.;
RL Submitted (DEC-2002) to Swiss-Prot.
CC -!- FUNCTION: ACTS AS A SERINE PROTEASE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR InterPro; IPR000209; Peptidase_S8.
DR PROSITE; PS00136; SUBTILASE ASP; PARTIAL.
DR PROSITE; PS00137; SUBTILASE HIS; PARTIAL.
DR PROSITE; PS00138; SUBTILASE_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 7
SQ SEQUENCE 7 AA; 688 MW; 776DD455A6C1AD80 CRC64;

Query Match 23.3%; Score 21; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SNAP 9
Db 4 SNAP 7

Search completed: June 3, 2004, 15:26:43
Job time : 39 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:15:29 ; Search time 53 seconds  
(without alignments)  
90.628 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_72  
Perfect score: 90  
Sequence: 1 QNILLSNAPLGQFPPT 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 459173

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	87.8	15	2	AAW15321 Class II
2	79	87.8	15	2	AAW71591 Class II
3	79	87.8	15	2	AAW85296 Helper T-
4	79	87.8	15	2	AAV40209 Amino aci
5	79	87.8	15	2	AAV33168 Human tyr
6	79	87.8	15	2	AAI26865 Melanoma-
7	79	87.8	15	2	AAV00710 Tumour an
8	79	87.8	15	2	AAV49658 Tumour an
9	79	87.8	15	2	AAV01748 Exemplary
10	79	87.8	15	3	AAV71515 Human Tyr
11	79	87.8	15	3	AAV13739 Peptide f
12	79	87.8	15	3	AAI92295 Tyrosinas
13	79	87.8	15	3	AAV84291 Tumour as
14	79	87.8	15	3	AAV82974 Tyrosinas
15	79	87.8	15	3	AAV02617 Tumour as
16	79	87.8	15	3	AAV08689 Antigenic
17	79	87.8	15	4	AAV99392 Vaccine r
18	79	87.8	15	4	AAV02106 Tyrosinas
19	79	87.8	15	4	AAV11349 Exemplary
20	79	87.8	15	4	AAV06836 Human tyr
21	79	87.8	15	5	ABG79139 Human tyr
22	79	87.8	15	5	AAV19078 HLA-DR4 r
23	79	87.8	15	6	AAV19543 Human can
24	78	86.7	15	2	AAW15337 Class II
25	78	86.7	15	4	AAV99403 Vaccine r

## ALIGNMENTS

## RESULT 1

AAW15321	15	4	AAV99390 Vaccine r
ID AAW15321 standard; peptide; 15 AA.	15	2	AAW15340 Class II
XX AC AAW15321;	15	2	AAW15326 Class II
XX 09-FEB-1998 (first entry)	15	4	AAV99394 Vaccine r
XX Class II restricted melanoma tyrosinase derived antigenic peptide 1.	15	4	AAV99402 Vaccine r
XX Major histocompatibility complex; MHC; Class II; tyrosinase; vaccine;	15	4	AAV99400 Vaccine r
XX immune response; immunogenic peptide; melanoma; treatment;	15	2	AAW15342 Class II
XX protective antibody; immune cells; CD8+ T cell; CD4+ T cell.	15	2	AAW15336 Class II
XX Synthetic.	15	2	AAW15328 Class II
XX Homo sapiens.	15	2	AAW15339 Class II
XX WO9711669-A2.	15	4	AAV99397 Vaccine r
XX 03-APR-1997.	15	4	AAV99389 Vaccine r
XX 25-SEP-1996; 96WO-US015346.	15	4	AAV99391 Vaccine r
XX 26-SEP-1995; 95US-00533895.	15	4	AAV99378 Vaccine r
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.	15	2	AAW15322 Class II
XX Topalian SL, Rosenberg SA, Robbins PF;	15	2	AAW15344 Class II
XX WPI; 1997-212652/19.	15	2	AAW15347 Class II
XX Major histocompatibility complex Class H immunogenic peptide - used to	15	2	AAW15341 Class II
XX prevent or treat melanoma in mammal by stimulating production of	15	2	AAW15338 Class II
XX protective antibodies or immune cells.	15	4	AAV99401 Vaccine r
XX Claim 2; Page 59; 79pp; English.			
XX Peptides AAW15321-56 are major histocompatibility complex (MHC) Class II			
XX restricted melanoma peptides, derived from tyrosinase. Tumour reactive			
XX human CD4+ and CD8+ T cells recognise melanoma antigens encoded by the			
XX tyrosinase gene. The present sequence is derived from amino acids 56-70.			
XX The peptides may be used as a vaccine, either prophylactically in advance			
XX of any evidence of melanoma, or therapeutically to enhance the patients			
XX own immune response. The immunogenic peptides can be used to prevent or			
XX treat melanoma in a mammal by stimulating the production of protective			
XX antibodies or immune cells, preferably immune positive CD4+ T cells			
XX Sequence 15 AA;			
SQ			

Query Match 87.8%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
 |||||  
 Db 1 QNILLSNAPLGQFPF 15

RESULT 2  
 AAW71591  
 ID AAW71591 standard; peptide; 15 AA.  
 XX  
 AC AAW71591;  
 XX  
 DT 24-NOV-1998 (first entry)  
 XX  
 DE Class II-restricted epitope.  
 XX  
 KW Hepatitis B surface antigen; HsAg; MHC class II-restricted peptide;  
 KW vaccination; vaccine; MHC class I molecule; immune response; cancer;  
 KW major histocompatibility complex molecule; pathogenic organism;  
 KW viral disease; autoimmune condition; allergy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9833523-A1.  
 XX  
 PD 06-AUG-1998.  
 XX  
 XX 02-FEB-1998; 98WO-GB000325.  
 XX  
 PR 31-JAN-1997; 97GB-00001999.  
 PR 05-JUL-1997; 97GB-00014182.  
 PR 07-AUG-1997; 97GB-00016620.  
 PR 07-AUG-1997; 97GB-00016641.  
 PR 21-NOV-1997; 97GB-00024584.  
 XX  
 PA (BIOV-) BIOVATION LTD.  
 XX  
 PI Carr FU, Carter G;  
 XX  
 XX WPI; 1998-437178/37.  
 XX  
 DR Immunogenic molecules - comprising nucleic acid and polypeptide portion,  
 PT from both of which peptide for presentation on major histocompatibility  
 PT complex molecules can be derived.  
 XX  
 XX Example 5; Page 49; 87pp; English.  
 PS  
 CC A molecule has been developed which comprises: (a) a nucleic acid portion  
 CC from which at least one peptide for presentation of MHC class I or class  
 CC II molecules, or both, may be derived, and (b) a polypeptide portion,  
 CC from which at least 1 peptide for presentation on MHC class I or class II  
 CC molecules, or both, may be derived. Also described in the present  
 CC invention is another molecule comprising: (a) a nucleic acid portion from  
 CC which at least 1 peptide for presentation on MHC class I or class II  
 CC molecules, or both, may be derived, and (b) a polypeptide portion  
 CC comprising a recognition domain capable of targeting the molecule to an  
 CC antigen presenting cell (APC), where the polypeptide portion does not  
 CC comprise a specific antigen binding site. The molecules can be used to  
 CC induce immune responses to treat or prevent, e.g. diseases caused by  
 CC pathogenic organisms, cancers, viral disease, e.g. HIV or hepatitis  
 CC infection, autoimmune conditions, e.g. Grave's disease, multiple  
 CC sclerosis, systemic lupus erythematosus, diabetes mellitus, Kawasaki's  
 CC disease, rheumatoid arthritis or allergies, e.g. atopic dermatitis,  
 CC allergic rhinitis, allergic conjunctivitis, atopic asthma or eczema. The  
 CC combination of DNA and polypeptide in the same molecule can give rise not  
 CC only to a combination of MHC class I- and MHC class II-mediated immune  
 CC responses but also to an enhancement of these responses compared to the  
 CC responses given by either DNA or polypeptide alone. The present sequence  
 CC represents an epitope used in an example from the present invention

XX SQ Sequence 15 AA;  
 Query Match 87.8%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
 |||||  
 Db 1 QNILLSNAPLGQFPF 15

RESULT 3  
 AAW85296  
 ID AAW85296 standard; peptide; 15 AA.  
 XX  
 AC AAW85296;  
 XX  
 DT 16-FEB-1999 (first entry)  
 XX  
 DE Helper T-cell class II peptide derived from a tyrosinase.  
 XX  
 KW Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;  
 KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;  
 KW acquired immune deficiency syndrome; malaria; cancer;  
 KW allograft rejection; allergy; Lyme disease; hepatitis;  
 KW post-streptococcal endocarditis; glomerulonephritis;  
 KW food hypersensitivity.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9832456-A1.  
 XX  
 PD 30-JUL-1998.  
 XX  
 XX 23-JAN-1998; 98WO-US001373.  
 PR 23-JAN-1997; 97US-0036713P.  
 PR 07-FEB-1997; 97US-0037432P.  
 XX  
 XX (EPIM-) EPIMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S;  
 XX  
 XX WPI; 1998-427679/36.  
 XX  
 DR Composition containing peptide that induces cytotoxic T lymphocyte  
 PT response, and helper peptide - can bind to human leucocyte antigen  
 PT alleles, used to treat or prevent cancers, parasitic infections and  
 PT autoimmune disease.  
 XX  
 PS Disclosure; Page 40; 51pp; English.  
 CC  
 CC AAW85284-451 represent helper T-cell class II peptides, which can bind to  
 CC the human leucocyte antigens (HLA) DR4w4, DR1 and DR7. The peptides are  
 CC used in the course of the invention. The specification describes peptides  
 CC that induce a cytotoxic T lymphocyte (CTL) response, and T-helper  
 CC peptides, that are used together to generate a CTL response for the  
 CC treatment or prevention of viral, fungal, bacterial or parasitic  
 CC infections (e.g. hepatitis, acquired immune deficiency syndrome or  
 CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate  
 CC cancer or condyloma acuminatum). Helper T-cell peptides may be used alone  
 CC to induce a helper T cell response, e.g. in cases of autoimmune disease,  
 CC allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal  
 CC endocarditis, glomerulonephritis and food hypersensitivity  
 XX  
 SQ Sequence 15 AA;  
 Query Match 87.8%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15



|||||  
1 QNILLSNAPLGQFP 15

Db

## RESULT 4

AAAY40209  
ID AAY40209 standard; peptide; 15 AA.

XX AC AAY40209;

XX DT 19-NOV-1999 (first entry)

XX DE Amino acid sequence of a human melanoma epitope.

XX KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;  
XX KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;  
XX KW vaccine; tumor; infection; immune response; cytokine profile;  
XX KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;  
XX KW autoimmune disease.

XX OS Homo sapiens.

XX FN FR2774687-A1.

XX PD 13-AUG-1999.

XX PF 06-FEB-1998; 98FR-00001439.

XX PR 06-FEB-1998; 98FR-00001439.

XX PA (INRM ) INSERM INST NAT SANTE &amp; RECH MEDICALE.

XX PA (INSP ) INST PASTEUR LILLE.

XX PI Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;

XX DR WPI; 1999-510734/43.

XX PT New lipopeptide comprising C-terminal interferon-gamma fragment with  
XX PT attached lipophilic groups, used as interferon mimic, e.g. for treating  
XX PT cancer or virus infection.

XX PS Disclosure; Page 35; 53pp; French.

XX CC AAY40123-X40379 represent epitopes that are able to activate cytotoxic T  
XX CC lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or B  
XX CC epitopes recognized by corresponding antibodies. The epitopes may be used  
XX CC in the composition of the invention. The specification describes a  
XX CC lipopeptide that has a peptide part derived from mammalian interferon  
XX CC gamma (IFN $\gamma$ ) and one or more lipophilic parts comprising a linear or  
XX CC branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The  
XX CC lipopeptide mimics the activity of IFN $\gamma$ . Compositions comprising the  
XX CC lipopeptide are used to treat or prevent any condition that responds to  
XX CC IFN $\gamma$ , and as adjuvant for vaccines (particularly those directed against  
XX CC tumors, viral or parasitic infections), to stimulate or reorient the  
XX CC immune response between types 1 and 2 cytokine profiles. Particular  
XX CC applications are treatment of infections (particularly viral, e.g.  
XX CC acquired immune deficiency syndrome, papilloma (cancer) and hepatitis,  
XX CC but also bacterial, fungal, parasitic or helminth); cancers (particularly  
XX CC of kidney, cutaneous T cells or ovary, chronic myelogenous leukemia or  
XX CC mesothelioma), allergy; and autoimmune diseases

XX SQ Sequence 15 AA;

Query Match 87.8%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15

Db 1 QNILLSNAPLGQFP 15

## RESULT 5

AAAY33168  
ID AAY33168 standard; peptide; 15 AA.

XX AC AAY33168;

XX DT 17-NOV-1999 (first entry)

XX DE Human tyrosinase peptide #7.

XX KW Human; protein delivery; Yersinia sp; effector gene; mutant; antigen;  
XX KW immune response; cytotoxic T-lymphocyte; CTL; vaccination; treatment;  
XX KW pathological disorder; tyrosinase.

XX OS Homo sapiens.

XX FN WO9945098-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-IB000587.

XX PR 06-MAR-1998; 98US-00036582.

XX PA (VBRU/) VAN DER BRUGGEN P B.

XX PA (CORN/) CORNELIS G R.

XX PA (BOLA/) BOLAND A M.

XX PA (BOON/) BOON-FALLEUR T R.

XX PI Van Der Bruggen PB, Cornelis GR, Boland AM, Boon-Falleur TR;

XX DR WPI; 1999-540840/45.

XX PT New mutant Yersinia strains useful for treating a pathological disorder.

XX PS Example 1 ; Page 70; 80pp; English.

XX CC This invention describes a novel mutant Yersinia (Y1) strain, comprising  
XX CC mutation(s) in effector-encoding gene(s) and deficient in the production  
XX CC of functional effector protein(s). The invention describes (1) a  
XX CC quintuple mutant Yersinia strain, having the designation Yersinia  
XX CC enterocolitica yopEHOMP or Yersinia pseudotuberculosis yopEHAOU; (2) an  
XX CC expression vector (EVI) for delivering a heterologous protein into a  
XX CC eukaryotic cell, comprising in the 5'-3' direction; (3) a Yersinia or  
XX CC mutant Yersinia strain for delivering a heterologous protein into a  
XX CC eukaryotic cell, comprising contacting the cell with a Y1 transformed  
XX CC cell with the above vector (Y1-EV1); (4) a method for delivering a  
XX CC heterologous protein into a eukaryotic cell, comprising contacting the  
XX CC cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method  
XX CC for inducing an immune response specific for a heterologous protein; (6)  
XX CC a method for inducing a cytotoxic T-lymphocyte (CTL) response specific  
XX CC for a heterologous protein; (7) a method for determining the efficacy of  
XX CC an antigen vaccination regimen in a subject. Y1 is used to treat a  
XX CC pathological disorder, by providing recombinant Yersinia for the safe  
XX CC delivery of proteins into eukaryotic cells. AAY33147-Y33178 are human-  
XX CC derived peptides used to illustrate the method of the invention

XX SQ Sequence 15 AA;

Query Match 87.8%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15

Db 1 QNILLSNAPLGQFP 15

## RESULT 6

AAY26865

ID AAY26865 standard; peptide; 15 AA.

XX AC AAY26865;

XX XX

DT 14-SEP-1999 (first entry)  
 XX Melanoma-derived lipopeptide epitope #6 for mixed micelles.  
 DE  
 XX  
 KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;  
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;  
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;  
 KW melanoma; Plasmodium falciparum; malaria.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX FR2771640-A1.  
 XX  
 XX 04-JUN-1999.  
 XX  
 XX 03-DEC-1997; 97FR-00015246.  
 XX  
 XX 03-DEC-1997; 97FR-00015246.  
 XX  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (INSP ) INST PASTEUR LILLE.  
 XX  
 XX Gras MH, Bossus M, Lippens G, Wierszeski JM, Tartar A;  
 PI Guillet JG, Bourgault VI;  
 XX WPI; 1999-349509/30.  
 XX  
 XX Immunogenic lipopeptide micelles - comprising lipopeptides containing  
 PT cytotoxic and helper T-lymphocyte epitopes.  
 XX  
 XX Disclosure; Page 37; 60pp; French.  
 XX  
 CC The invention relates to the generation of mixed micelles or  
 CC microaggregates for inducing an immune response comprise: (a) a first  
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope  
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at  
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit  
 CC different from that of the first lipopeptide. This peptide represents an  
 CC example of a lipopeptide epitope used in the invention and is derived  
 CC from a human melanoma protein. The immunogenic lipopeptide micelles are  
 CC used in vaccines, especially against HIV, hepatitis B virus (HBV),  
 CC papilloma viruses, p53, melanoma or Plasmodium falciparum malaria  
 XX  
 SQ Sequence 15 AA;  
 Query Match 87.8%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQFP 15  
 DB 1 QNILLSNAPLGQFP 15  
 RESULT 7  
 AAY00710  
 ID AAY00710 standard; peptide; 15 AA.  
 XX  
 AC AAY00710;  
 XX  
 XX 12-MAY-1999 (first entry)  
 XX  
 XX Tumour antigen booster peptide Tyrosinase HLA-DR4.  
 XX  
 KW Tumour antigen; booster peptide; immune response modulation; allergy;  
 KW immune response enhancer; tumour cell; tumour rejection antigen;  
 KW leukocyte antigen-presenting molecule; autoimmune disease;  
 KW allograft rejection.  
 XX  
 XX Homo sapiens.  
 OS  
 XX

PN WO958956-A2.  
 XX  
 PD 30-DEC-1998.  
 XX  
 XX 19-JUN-1998; 98WO-US012894.  
 PF  
 XX 23-JUN-1997; 97US-00880979.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 XX Warnier G, Uyttenhove C, Boon-Falleur T;  
 PI WPI; 1999-105612/09.  
 DR  
 XX  
 XX Immunization methods using viruses expressing antigen for priming and  
 PT booster immunizations - useful for modulating immune responses against  
 PT antigen, e.g. enhancing immune response against tumour cells expressing  
 PT tumour rejection antigens.  
 XX  
 XX Disclosure; Page 9; 33pp; English.  
 XX  
 CC This sequence represents a tumour antigen booster peptide that can be  
 CC used in the method of the invention. The method is for for modulating an  
 CC immune response in a mammal against an antigen, and comprises: (A)  
 CC inducing an immune response by: (i) administering a virus containing a  
 CC nucleic acid molecule encoding the antigen or its precursor to generate  
 CC an immune response; and (ii) administering at least one booster dose  
 CC comprising a peptide including the antigen, in an adjuvant, in a combined  
 CC amount effective to enhance the initial immune response; or (B) reducing  
 CC an immune response as defined for (A) but using a non-adjuvant with the  
 CC peptide which includes the antigen, in an amount effective to reduce the  
 CC initial immune response. Method (A) is used to enhance the immune  
 CC response against tumour cells expressing tumour rejection antigens, and  
 CC against pathogens in subjects having human leukocyte antigen-presenting  
 CC molecules. Method (B) is used to reduce the immune response in allergy,  
 CC autoimmune disease, and allograft rejection. Method (A) provides an  
 CC immunisation method which, unlike prior art, is not limited by the host  
 CC immune response against viral vectors  
 XX  
 SQ Sequence 15 AA;  
 Query Match 87.8%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQFP 15  
 DB 1 QNILLSNAPLGQFP 15  
 RESULT 8  
 AAY49658  
 ID AAY49658 standard; peptide; 15 AA.  
 XX  
 AC AAY49658;  
 XX  
 XX 14-JAN-2000 (first entry)  
 XX  
 XX Tumour antigenic peptide SEQ ID NO:25.  
 DE  
 XX  
 KW Human; sdp3.10; SAGE; sdp3.8; HAGE; sdp3.5; TRAP; sarcoma;  
 KW tumour rejection antigen precursor; tumour associated nucleic acid;  
 KW carcinoma; cancer; immune response; diagnosis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9953061-A2.  
 PN  
 XX 21-OCT-1999.  
 PD  
 XX 14-APR-1999; 99WO-US008163.  
 PF  
 XX 15-APR-1998; 98US-00060706.  
 PR

PR 27-JUL-1998; 98US-00122989.  
PR 30-OCT-1998; 98US-00183706.  
PR 30-OCT-1998; 98US-00183789.  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX Martelange V, De Smet C, Boon-Falleur T;  
PI WPI; 1999-620430/53.  
XX  
XX New nucleic acid encoding sarcoma-associated gene products, useful for  
PT diagnosing, e.g. treating and preventing cancer.  
PT Disclosure; Page 25; 93pp; English.  
XX  
XX The present invention describes sarcoma-associated gene products (I).  
CC Agents, specifically sarcoma associated nucleic acids (II) or their  
CC expression products that are tumour rejection antigens (TNA), that  
CC selectively increase formation of HLA (human leucocyte antigen)/(I)  
CC complexes are used for treating cancer, especially sarcoma and carcinoma,  
CC in humans and other animals. Compositions containing autologous cytolytic  
CC T cells (CTL), specific for the HLA/I complex, are similarly useful,  
CC also transformed cells that stimulate such CTL in vivo. (II) are also  
CC used: (i) as source of therapeutic antisense sequences that reduce  
CC expression of (II); (ii) for recombinant production of (I); (iii)  
CC particularly its fragments, as primers and probes in usual hybridisation  
CC and amplification assays, for diagnosis, prognosis and monitoring of  
CC tumours, or for measuring binding specificity of HLA molecules or CTL  
CC clones; (iv) to identify related sequences; and (v) for generating  
CC transgenic animals, e.g. for studying cancer and immune responses to it.  
CC (I) are used to raise specific antibodies (Ab) and therapeutically. Ab  
CC are used to diagnose tumours in immunoassays, also for delivering drugs,  
CC toxins, imaging agents etc. to (I)-expressing cells. AAY49637 to AAY49670  
CC represent exemplary tumour antigenic peptides given in the present  
CC invention  
XX  
XX Sequence 15 AA;  
SQ

Query Match 87.8%; Score 79; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
| | | | | | | | | | | | | | |  
Db 1 QNILLSNAPLGQPP 15  
| | | | | | | | | | | | | | |

RESULT 9  
AAY01748  
ID AAY01748 standard; peptide; 15 AA.  
XX  
XX AC AAY01748;  
XX  
XX DT 25-JUN-1999 (first entry)  
XX  
XX DE Exemplary antigenic peptide derived from Tyrosinase.  
XX  
XX KW MAGE-3; tumour associated gene; human leucocyte antigen Class II;  
KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;  
KW osteosarcoma; leukemia; carcinoma.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO9914326-A1.  
XX  
XX PD 25-MAR-1999.  
XX  
XX PF 04-SEP-1998; 98WO-US018601.  
XX  
XX PR 12-SEP-1997; 97US-00928615.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA (UYVR-) UNIV VRIJE BRUSSEL.

XX Thielemans K, Heirman C, Corthals J, Chau P, Stroobant V;  
PI Boon-Falleur T, Van Der Bruggen P, Luiten R;  
XX WPI; 1999-244031/20.  
XX  
XX Isolated peptides that bind to human leucocyte antigen class II  
PT molecules.  
XX  
XX Disclosure; Page 29; 88pp; English.  
XX  
XX The present sequence represents an exemplary tumour associated peptide  
CC antigen. The specification describes a MAGE-3 tumour associated gene.  
CC Peptides (AAY01721-25) that bind human leucocyte antigen (HLA) Class II  
CC molecules can be derived from the MAGE-3 protein. These peptides and  
CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide and HLA  
CC Class II, are used to treat MAGE-3 related diseases, particularly cancers  
CC (e.g. melanoma, osteosarcoma, leukemia and various forms of carcinoma).  
CC The peptides are also used to produce specific antibodies. Detection of  
CC of the peptides, e.g. in binding assays, particularly with antibodies, is  
CC used for diagnosis of such diseases  
XX  
XX Sequence 15 AA;  
SQ

Query Match 87.8%; Score 79; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
| | | | | | | | | | | | | | |  
Db 1 QNILLSNAPLGQPP 15  
| | | | | | | | | | | | | | |

RESULT 10  
AAY71515  
ID AAY71515 standard; peptide; 15 AA.  
XX  
XX AC AAY71515;  
XX  
XX DT 12-OCT-2000 (first entry)  
XX  
XX DE Human Tyrosinase peptide-5.  
XX  
XX KW Tyrosinase; human; Tumour Rejection Antigen; TRA; tumour; cancer; HLA;  
KW Human Leucocyte Antigen; MHC; Major Histocompatibility Complex; CTL;  
KW cytolytic T-lymphocyte; immune response stimulator; prophylaxis; therapy;  
KW diagnosis; TNF; tumour necrosis factor; vaccine; cytostatic.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200032769-A2.  
XX  
XX PD 08-JUN-2000.  
XX  
XX PF 26-NOV-1999; 99WO-IB002018.  
XX  
XX PR 27-NOV-1998; 98GB-00026143.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX Huang L, Van Pel A, Braeser F, De Plaen E, Boon T;  
PI WPI; 2000-412317/35.  
XX  
XX Novel polypeptides expressed in tumor cells useful for treating cancers  
PT have an ability to complex with a major histocompatibility complex  
PT molecule and comprises a specific unbroken amino acid sequence.  
XX  
XX Disclosure; Page 19; 80pp; English.  
XX  
XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and  
CC decapeptide sequences, that function as tumour rejection antigens (TRAS).  
CC These peptides are capable of forming a complex with major

CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte  
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune  
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune  
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,  
 CC therapy and diagnosis of tumours and are effective in controlling or  
 CC preventing tumour growth. The present sequence is the human tyrosinase  
 CC peptide-5, that corresponds to residues 56-70 of the tumour associated  
 CC gene, tyrosinase encoding protein. It can be administered to induce or  
 CC enhance an immune response and is presented by HLA-DR4 complex. This  
 CC peptide can serve as a tumour rejection antigen (TRA) and in combination  
 CC with adjuvants, can produce vaccines useful for treating a variety of  
 CC tumours  
 XX  
 SQ Sequence 15 AA;  
 Query Match 87.8%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGPOPP 15  
 Db 1 QNILLSNAPLGPOPP 15  
 RESULT 11  
 AAB13739  
 ID AAB13739 standard; peptide; 15 AA.  
 AC AAB13739;  
 XX  
 DT 02-FEB-2001 (first entry)  
 DE Peptide fragment # 5 from human tyrosinase.  
 XX  
 KW Human; T-cell; immune response; antigen; epitope; B7 family molecule;  
 KW Leukocyte function-associated antigen-3; LFA-3;  
 KW Intercellular adhesion molecule-1; ICAM-1; vaccine; immunotherapy;  
 KW colon polyp; Crohn's disease; ulcerative colitis; breast lesion; tumour;  
 KW tyrosinase.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200034494-A1.  
 XX  
 PD 15-JUN-2000.  
 XX  
 PF 12-NOV-1999; 99WO-US026866.  
 XX  
 PR 09-DEC-1998; 98US-0111582P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (THER-) THERION BIOLOGICS CORP.  
 XX  
 PI Schlom J, Hodge J, Panicali D;  
 XX  
 DR WPI; 2000-431307/37.  
 XX  
 PT Novel recombinant vector useful as immunogens and vaccines for  
 PT stimulating and enhancing immunological responses to target cells and  
 PT antigens expresses multiple co-stimulatory molecules such as B7-1, LFA-3,  
 PT ICAM-1.  
 XX  
 PS Claim 18; Page 35; 188pp; English.  
 XX  
 CC Costimulatory molecules have important roles in T-cell activation and  
 CC therefore the immune response. The present invention relates to  
 CC recombinant vectors which comprise of foreign nucleic acid sequences  
 CC encoding at least three costimulatory molecules: a B7 family molecule,  
 CC leukocyte function-associated antigen-3 (LFA-3, human CD58) and  
 CC intercellular adhesion molecule-1 (ICAM-1, CD54) and optionally a foreign  
 CC gene encoding a target antigen or immunological epitope. The present  
 CC sequence is one such target antigen or immunological epitope. The present  
 CC present sequence is a tumour-associated antigen. The vector of the

CC present invention would be useful for providing an enhanced immune  
 CC response to the present target antigen. The vector of the present  
 CC invention may therefore be useful in immunotherapy for treating or  
 CC preventing diseases caused by viruses, bacteria, protozoans, parasites,  
 CC premalignant cells and tumour cells. The recombinant vector can be used  
 CC to treat or prevent preneoplastic or hyperplastic states such as colon  
 CC polyps, Crohn's disease, ulcerative colitis and breast lesions  
 XX  
 SQ Sequence 15 AA;  
 Query Match 87.8%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGPOPP 15  
 Db 1 QNILLSNAPLGPOPP 15  
 RESULT 12  
 AAY92295  
 ID AAY92295 standard; peptide; 15 AA.  
 XX  
 AC AAY92295;  
 XX  
 DT 10-AUG-2000 (first entry)  
 DE Tyrosinase antigenic peptide epitope (residues 56-70).  
 XX  
 KW Tyrosinase; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;  
 KW human leukocyte antigen; HLA.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200020445-A2.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 15-SEP-1999; 99WO-IB001664.  
 XX  
 PR 02-OCT-1998; 98US-00165863.  
 PR 09-APR-1999; 99US-00289350.  
 XX  
 PA (CHAU/) CHAUX P.  
 PA (LUIT/) LUITEN R.  
 PA (DEMO/) DEMOTTE N.  
 PA (DUFF/) DUFFOUR M.  
 PA (LURO/) LURQUIN C.  
 PA (TRAV/) TRAVERSARI C.  
 PA (STRO/) STROOBANT V.  
 PA (CORN/) CORNELIS G R.  
 PA (BOON/) BOON-FALLEUR T.  
 PA (VERU/) VAN DER BRUGGEN P.  
 PA (SCHU/) SCHULTZ E.  
 PA (WARN/) WARNIER G.  
 XX  
 PI Chau P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;  
 PI Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;  
 PI Schultz E, Warnier G;  
 XX  
 DR WPI; 2000-303739/26.  
 XX  
 PT Isolation of cytotoxic T-lymphocytes clones by successive steps of  
 PT stimulation and testing of lymphocytes with antigen presenting cells  
 PT which present antigens derived from different expression systems.  
 XX  
 PS Disclosure; Page 22; 99pp; English.  
 XX  
 CC A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones  
 CC comprises successive steps of stimulation and testing of lymphocytes with  
 CC antigen presenting cells (APCs) which present antigens derived from  
 CC different expression systems. The CTL clones isolated recognize specific  
 CC antigenic peptides of proteins, preferably of the MAGE family. The APC is

CC autologous and each expression systems is different from at least one of  
 CC the other expression systems, therefore isolating a cytotoxic T cell  
 CC clone specific for the protein. The method can also be used to identify  
 CC an antigenic peptide epitope. Isolated CTL clones specific for a  
 CC peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells  
 CC specific for the complexes, peptides or cells which present the complexes  
 CC on the cell surface are useful for treating pathological conditions  
 CC characterized by abnormal expression of the complexes  
 XX  
 XX Sequence 15 AA;

SQ

Query Match 87.8%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
 DB 1 QNILLSNAPLGQFPF 15

RESULT 13

AY84291  
 ID AAY84291 standard; peptide; 15 AA.

XX

AC AAY84291;

XX

DT 12-JUL-2000 (first entry)

XX

DE Tumour associated antigen derived from tyrosinase.

XX

KW tumour rejection antigen; macrophage colony stimulating gene;  
 KW macrophage-colony stimulating factor; antigen presenting cell;  
 KW human leukocyte antigen; CD8+ cytotoxic T lymphocyte.

XX

OS Homo sapiens.

XX

PN WO200013699-A1.

XX

PD 16-MAR-2000.

XX

PF 03-SEP-1999; 99WO-US020344.

XX

PR 04-SEP-1998; 98US-0099077P.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Probst-Kepper M, Van Den Eynde B, Boon-Falleur T;

XX

DR WPI; 2000-256859/22.

XX

PT Isolated polypeptide used to treat subjects having a disorder  
 PT characterized by expression of alternative open reading frame macrophage-  
 PT colony stimulating factor comprises 25 amino acid residue sequence.

XX

PS Disclosure; Page 20; 74pp; English.

XX

CC AAY84270-Y84303 represent peptides which are tumour associated antigens.  
 CC They can be administered in conjunction with the tumour rejection antigen  
 CC precursor of the invention to induce anti-tumour responses. The tumour  
 CC rejection antigen precursor of the invention is encoded by an alternative  
 CC open reading frame (ORF) of human macrophage colony stimulating gene.  
 CC Peptides derived from the alternative ORF of macrophage-colony  
 CC stimulating factor, when presented by an antigen presenting cell having a  
 CC human leukocyte antigen (HLA) class I molecule, effectively induce the  
 CC activation and proliferation of CD8+ cytotoxic T lymphocytes. Polypeptide  
 CC and nucleic acids derived from the alternate ORF of macrophage-colony  
 CC stimulating factor are useful for enriching selectively a population of T  
 CC lymphocytes with CD8+ T lymphocytes. They are also useful for diagnosing  
 CC a disorder characterized by expression of the polypeptide, and for  
 CC identifying functional variants and mimetics

XX

SQ Sequence 15 AA;

Query Match

Best Local Similarity 87.8%; Score 79; DB 3; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15

DB 1 QNILLSNAPLGQFPF 15

RESULT 14

AY82974

ID AAY82974 standard; peptide; 15 AA.

XX

AC AAY82974;

XX

DT 19-JUN-2000 (first entry)

XX

DE Tyrosinase tumour associated antigen.

XX

KW Tumour; tumour associated antigen; retrovirus; antisense; treatment;  
 KW probe; primer; HLA; cytotoxic T-lymphocyte; cancer; testis; antibody;  
 KW CTL; helper T-lymphocyte; MAGE; GAGE; RAGE; Gnt-V; MUM; CDK4;  
 KW beta catenin; tyrosinase; Melan-A; gp100; PRAME.

XX

OS Homo sapiens.

XX

PN WO200006598-A1.

XX

PD 10-FEB-2000.

XX

PF 15-JUL-1999; 99WO-US016236.

XX

PR 29-JUL-1998; 98US-00124398.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Coulie P, Boon-Falleur T;

XX

DR WPI; 2000-205453/18.

XX

PT Novel nucleic acids encoding melanoma associated gene products and their  
 PT fragments and variants, useful for treating endogenous retrovirus  
 PT mediated tumors, especially melanomas.

XX

PS Disclosure; Page 26; 77pp; English.

XX

CC Tumor associated disorders (e.g. endogenous retrovirus mediated tumors,  
 CC especially melanomas) can be treated or ameliorated by administering  
 CC antisense nucleic acid to reduce the expression of tumour associated  
 CC genes such as HERV-AVL3-B. Progression of a disorder characterized by the  
 CC expression of the HERV-AVL3-B endogenous retrovirus tumor rejection  
 CC antigen (ERTRA) can be diagnosed or monitored by contacting a non-testis  
 CC biological sample with an agent that binds to the complex and determining  
 CC the interaction. A disorder can also be treated by administering an agent  
 CC that enriches the presence of HLA and HERV-AVL3-B ERTRA or by  
 CC administering autologous cytotoxic T-cells sufficient to ameliorate the  
 CC disorder. Fragments of the HERV-AVL3-B coding sequence are useful as  
 CC probes or amplification primers for determining the expression of HERV-  
 CC AVL3-B genes, to express tumor associated polypeptides in vivo and in  
 CC vitro and to prepare fragments of such polypeptides to synthesize  
 CC antibodies. Antigenic peptides of HERV-AVL3-B can be useful for  
 CC generating antibodies either alone or as fusion proteins, as components  
 CC of immunoassay and for determining the binding specificity of HLA  
 CC molecules and/or cytotoxic T lymphocyte (CTL) for HERV-AVL3-B proteins.  
 CC Peptides derived from the HERV-AVL3-B coding sequence and which are  
 CC presented by MHC molecules and recognised by CTL or helper T-lymphocytes  
 CC can be combined with peptides from other tumour rejection antigens by  
 CC preparation of hybrid nucleic acids or polypeptides to produce polytopes.  
 CC This exemplary tumour associated peptide antigen corresponds to amino  
 CC acids 56-70 of the tyrosinase polypeptide. See also AAY82953-Y82986

XX

SQ Sequence 15 AA;

Query Match 87.8%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
Db 1 QNILLSNAPLGQFP 15

## RESULT 15

AAB02617  
ID AAB02617 standard; peptide; 15 AA.

XX AC AAB02617;

XX DT 18-AUG-2000 (first entry)

XX DE Tumour associated peptide antigen from Tyrosinase #6.

XX KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;  
XX KM cancer; human; tumour; tumour associated gene product.

XX OS Homo sapiens.

XX PN WC200020581-A1.

XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-US021230.

XX PR 05-OCT-1998; 98US-00166448.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI (UYVR-) UNIV VRIJE BRUSSEL.

XX PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;  
XX PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;  
XX PI Heirman C;

XX DR WPI; 2000-317713/27.

XX PT New MAGE-A3 class II binding peptides, useful to diagnose and treat  
XX PT tumors, are fragments of MAGE-A3 which bind to and are presented to T  
XX PT lymphocytes by human leukocyte antigen class II molecules.

XX PS Disclosure; Page 33; 119pp; English.

XX CC The present invention relates to MAGE-A3 (tumour associated gene product)  
XX CC human leukocyte antigen (HLA) class II-binding peptides (see AAB02566-  
XX CC B02595, and AAB02633-B02637). These peptides are presented to T cells in  
XX CC the context of HLA class II molecules. The peptides stimulate the  
XX CC activity and proliferation of CD4+ T lymphocytes. The invention also  
XX CC includes nucleotide sequences encoding MAGE-3a peptides (see AAA37928 and  
XX CC AAA37938-A37940). The peptides and nucleotide sequences can be used to  
XX CC create antibodies against the MAGE-A3 peptides, the antibodies, peptides  
XX CC and nucleotide sequences can be used to create a vaccine. The peptides  
XX CC are used to diagnose or treat a disorder characterized by expression of  
XX CC MAGE-3, particularly cancer. The methods can also be used in the  
XX CC diagnosis of disorders associated with MAGE-3 expression. Included in the  
XX CC invention are other human tumour antigens (see AAB02596-B02637), and PCR  
XX CC primers used in the course of the invention (see AAA37929-A37937 and  
XX CC AAA37941-A37942)

XX SQ Sequence 15 AA;

Query Match 87.8%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
Db 1 QNILLSNAPLGQFP 15

Search completed: June 3, 2004, 15:25:28  
Job time : 54 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:26:51 ; Search time 42 Seconds  
(without alignments)  
113.875 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_72  
Perfect score: 90  
Sequence: 1 QNILLSNAPLGQFPPT 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 28138677 residues

Total number of hits satisfying chosen parameters: 206991

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/FCF\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/FCFUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	87.8	15	9 US-09-923-831-25	Sequence 25, Appl
2	79	87.8	15	9 US-09-766-889A-37	Sequence 37, Appl
3	79	87.8	15	12 US-10-218-095-32	Sequence 32, Appl
4	79	87.8	15	12 US-10-253-286-500	Sequence 500, App
5	79	87.8	15	12 US-10-103-395-198	Sequence 198, App
6	79	87.8	15	14 US-10-161-097-24	Sequence 24, Appl
7	79	87.8	15	14 US-10-170-832-66	Sequence 66, Appl
8	79	87.8	15	14 US-10-239-313A-495	Sequence 495, App
9	79	87.8	15	15 US-10-245-871-500	Sequence 500, App
10	79	87.8	15	15 US-10-406-317-13	Sequence 13, Appl
11	79	87.8	15	16 US-10-297-168-13	Sequence 13, Appl
12	78	86.7	15	14 US-10-239-313A-506	Sequence 506, App
13	77	85.6	15	14 US-10-239-313A-493	Sequence 493, App
14	76	84.4	15	14 US-10-239-313A-497	Sequence 497, App
15	76	84.4	15	14 US-10-239-313A-503	Sequence 503, App

16	76	84.4	15	14 US-10-239-313A-505	Sequence 505, App
17	75	83.3	15	14 US-10-239-313A-481	Sequence 481, App
18	75	83.3	15	14 US-10-239-313A-492	Sequence 492, App
19	75	83.3	15	14 US-10-239-313A-494	Sequence 494, App
20	75	83.3	15	14 US-10-239-313A-500	Sequence 500, App
21	73	81.1	15	14 US-10-239-313A-496	Sequence 496, App
22	73	81.1	15	14 US-10-239-313A-502	Sequence 502, App
23	73	81.1	15	14 US-10-239-313A-504	Sequence 504, App
24	71	78.9	15	14 US-10-239-313A-498	Sequence 498, App
25	70	77.8	15	14 US-10-239-313A-499	Sequence 499, App
26	66	73.3	13	9 US-09-847-185-41	Sequence 41, Appl
27	66	73.3	13	14 US-10-224-286-41	Sequence 41, Appl
28	43	47.8	9	14 US-10-219-850-21	Sequence 21, Appl
29	43	47.8	9	15 US-10-353-678-27	Sequence 27, Appl
30	33	36.7	14	10 US-09-880-748-2371	Sequence 2371, Ap
31	33	36.7	14	10 US-09-880-748-2615	Sequence 2615, Ap
32	33	36.7	14	12 US-10-293-418-2371	Sequence 2371, Ap
33	33	36.7	14	12 US-10-293-418-2615	Sequence 2615, Ap
34	32	35.6	13	14 US-10-224-999A-3214	Sequence 3214, Ap
35	32	35.6	14	10 US-09-880-748-2603	Sequence 2603, Ap
36	32	35.6	14	12 US-10-293-418-2603	Sequence 3224, Ap
37	32	35.6	14	14 US-10-224-999A-3224	Sequence 3224, Ap
38	32	35.6	14	14 US-10-224-999A-3225	Sequence 3225, Ap
39	32	35.6	15	14 US-10-224-999A-3235	Sequence 3235, Ap
40	32	35.6	15	14 US-10-224-999A-3236	Sequence 3236, Ap
41	32	35.6	15	14 US-10-224-999A-3237	Sequence 3237, Ap
42	32	35.6	16	14 US-10-224-999A-3247	Sequence 3247, Ap
43	32	35.6	16	14 US-10-224-999A-3248	Sequence 3248, Ap
44	32	35.6	16	14 US-10-224-999A-3249	Sequence 3249, Ap
45	32	35.6	16	14 US-10-224-999A-3250	Sequence 3250, Ap

## ALIGNMENTS

RESULT 1  
US-09-923-831-25  
; Sequence 25, Application US/09923831  
; Patent No. US20020115142A1  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val,rie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7034  
; CURRENT APPLICATION NUMBER: US/09/923.831  
; PRIOR FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 09/183,706  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-831-25

Query Match 87.8%; Score 79; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
Db 1 QNILLSNAPLGQFP 15

RESULT 2  
US-09-766-889A-37  
; Sequence 37, Application US/09766889A  
; Patent No. US20020164654A1  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre



; APPLICANT: Stroobant, Vincent  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: Schultz, Erwin  
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
; FILE REFERENCE: L0461/7104  
; CURRENT APPLICATION NUMBER: US/09/766,889A  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US 60/177,242  
; PRIOR FILING DATE: 2000-01-20  
; PRIOR APPLICATION NUMBER: US 60/243,212  
; PRIOR FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-766-889A-37

Query Match 87.8%; Score 79; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

RESULT 3  
US-10-218-095-32  
; Sequence 32, Application US/10218095  
; Publication No. US20040033541A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Yi  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Russo, Vincenzo  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF  
; FILE REFERENCE: L00461/70137  
; CURRENT APPLICATION NUMBER: US/10/218,095  
; CURRENT FILING DATE: 2002-08-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-218-095-32

Query Match 87.8%; Score 79; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

RESULT 4  
US-10-253-286-500  
; Sequence 500, Application US/10253286  
; Publication No. US20040058881A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2015  
; CURRENT APPLICATION NUMBER: US/10/253,286  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813

; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 500  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-253-286-500

Query Match 87.8%; Score 79; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

RESULT 5  
US-10-103-395-198  
; Sequence 198, Application US/10103395  
; Publication No. US20020160019A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR  
; TITLE OF INVENTION: RESTRICTED EPITOPES  
; FILE REFERENCE: 39963-20016.01  
; CURRENT APPLICATION NUMBER: US/10/103,395  
; CURRENT FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: US 09/009,953  
; PRIOR FILING DATE: 1998-01-21  
; PRIOR APPLICATION NUMBER: PCT/US98/01373  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: US 60/036,713  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: US 60/037,432  
; PRIOR FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 198  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-103-395-198

Query Match 87.8%; Score 79; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

RESULT 6  
US-10-161-097-24  
; Sequence 24, Application US/10161097  
; Publication No. US20030096404A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENZWEIG, Michael  
; APPLICANT: PYKETT, Mark J.  
; APPLICANT: SCADDEN, David T.  
; APPLICANT: POZNANSKY, Mark C.  
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
; TITLE OF INVENTION: DEVICES  
; FILE REFERENCE: C1005/7012/KA/ERG  
; CURRENT APPLICATION NUMBER: US/10/161,097  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US/09/574,749



; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/107,972  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: PCT/US99/26795  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/524,749  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Homo sapiens source  
US-10-161-097-24

Query Match 87.8%; Score 79; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQFP 15  
| | | | | | | | | | | | | | |  
Db 1 QNILLSNAPLGPQFP 15

## RESULT 7

US-10-170-832-66  
; Sequence 66, Application US/10170832  
; Publication No. US20030170792A1  
; GENERAL INFORMATION:  
; APPLICANT: Chau, Pascal  
; APPLICANT: Vantomme, Valrie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Corthals, Jurgen  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/10/170,832  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US/09/166,448  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-832-66

Query Match 87.8%; Score 79; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQFP 15  
| | | | | | | | | | | | | | |  
Db 1 QNILLSNAPLGPQFP 15

## RESULT 8

US-10-239-313A-495  
; Sequence 495, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID

; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 495  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-495

Query Match 87.8%; Score 79; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQFP 15  
| | | | | | | | | | | | | | |  
Db 1 QNILLSNAPLGPQFP 15

## RESULT 9

US-10-245-871-500  
; Sequence 500, Application US/10245871  
; Publication No. US20030235594A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2013  
; CURRENT APPLICATION NUMBER: US/10/245,871  
; CURRENT FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 500  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-245-871-500

Query Match 87.8%; Score 79; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQFP 15  
| | | | | | | | | | | | | | |  
Db 1 QNILLSNAPLGPQFP 15

## RESULT 10

US-10-406-317-13  
; Sequence 13, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
; molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE  
US-10-406-317-13

Query Match 87.8%; Score 79; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

RESULT 11  
US-10-297-168-13  
; Sequence 13, Application US/10297168  
; Publication No. US20040091995A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, Jeffrey  
; APPLICANT: GREINER, John W.  
; APPLICANT: KASS, Erik  
; APPLICANT: PANICALI, Dennis  
; TITLE OF INVENTION: RECOMBINANT NON-REPLICATING VIRUS EXPRESSING GM-CSF AND  
; TITLE OF INVENTION: USES THEREOF TO ENHANCE IMMUNE RESPONSES  
; FILE REFERENCE: 38163-0167  
; CURRENT APPLICATION NUMBER: US/10/297,168  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: PCT/US01/19201  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US60/211,717  
; PRIOR FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-297-168-13

Query Match 87.8%; Score 79; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

RESULT 12  
US-10-239-313A-506  
; Sequence 506, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711

; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 506  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-506

Query Match 86.7%; Score 78; DB 14; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.9e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

RESULT 13  
US-10-239-313A-493  
; Sequence 493, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 493  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-493

Query Match 85.6%; Score 77; DB 14; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.8e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

RESULT 14  
US-10-239-313A-497  
; Sequence 497, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23

; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 497  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-497

Query Match 84.4%; Score 76; DB 14; Length 15;  
Best Local Similarity 93.3%; Pred. No. 3.9e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQFP 15  
|||:|||||  
DB 1 QNILLSNAPVGPQFP 15

## RESULT 15

US-10-239-313A-503  
; Sequence 503, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 503  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-503

Query Match 84.4%; Score 76; DB 14; Length 15;  
Best Local Similarity 93.3%; Pred. No. 3.9e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQFP 15  
|||:|||||  
DB 1 QNILLSNAPVGPQFP 15

Search completed: June 3, 2004, 15:32:22  
Job time : 42 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:24:30 ; Search time 23 Seconds  
(without alignments)  
38.158 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_72

Perfect score: 90

Sequence: 1 QNILLSNAPLGQFPPT 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 152138

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/iaa/ECTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	87.8	15	2	US-09-036-582-22
2	79	87.8	15	3	US-09-183-706-25
3	79	87.8	15	3	US-09-166-448-66
4	79	87.8	15	4	US-09-567-995-25
5	79	87.8	15	4	US-09-163-863-22
6	79	87.8	15	4	US-09-009-953-198
7	79	87.8	15	4	US-09-697-884-66
8	79	87.8	15	4	US-09-289-350-22
9	79	87.8	15	4	US-09-574-749B-24
10	79	87.8	15	4	US-09-318-141-22
11	79	87.8	15	4	US-09-601-729-112
12	72	80.0	15	4	US-09-169-717E-28
13	66	73.3	13	2	US-08-902-516-41
14	66	73.3	13	4	US-09-847-185-41
15	33	36.7	10	3	US-08-159-339A-783
16	33	36.7	10	3	US-08-159-339A-747
17	31	34.4	9	2	US-08-725-736D-13
18	31	34.4	9	3	US-09-162-368B-13
19	31	34.4	9	3	US-09-161-877B-13
20	31	34.4	9	4	US-09-311-784A-402
21	31	34.4	10	1	US-08-461-005-1
22	31	34.4	10	2	US-07-930-685-1
23	30	33.3	15	4	US-09-311-784A-411
24	30	33.3	15	3	US-08-787-091-4
25	30	33.3	16	3	US-08-787-091-16
26	30	33.3	16	4	US-09-461-325-515
27	30	33.3	16	4	US-10-012-542-515

28	29	32.2	15	1	US-08-330-599-12	Sequence 12, Appl
29	29	32.2	16	3	US-08-602-999A-206	Sequence 206, App
30	29	32.2	16	4	US-09-500-124-206	Sequence 206, App
31	28	31.1	13	4	US-08-766-596A-40	Sequence 40, Appl
32	28	31.1	15	3	US-08-928-213B-18	Sequence 18, Appl
33	28	31.1	15	3	US-08-743-168B-15	Sequence 15, Appl
34	28	31.1	15	5	PCT-US96-10435-15	Sequence 15, Appl
35	28	31.1	16	3	US-08-405-647B-11	Sequence 11, Appl
36	28	31.1	16	3	US-08-985-499-11	Sequence 11, Appl
37	28	31.1	16	5	PCT-US96-03180-11	Sequence 11, Appl
38	27	30.0	8	4	US-09-561-500-42	Sequence 42, Appl
39	27	30.0	8	4	US-09-561-108-42	Sequence 42, Appl
40	27	30.0	8	4	US-09-561-526-42	Sequence 42, Appl
41	27	30.0	8	4	US-09-561-499-42	Sequence 42, Appl
42	27	30.0	8	4	US-09-998-831-42	Sequence 42, Appl
43	27	30.0	11	2	US-08-835-231-2	Sequence 2, Appl
44	27	30.0	11	3	US-09-108-661-2	Sequence 2, Appl
45	27	30.0	12	2	US-08-898-865-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-09-036-582-22  
; Sequence 22, Application US/09036582A  
; Patent No. 5965381  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Cornelis, Guy R.  
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
; FILE REFERENCE: 11154  
; CURRENT APPLICATION NUMBER: US/09/036,582A  
; CURRENT FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 39  
; SEQ ID NO 22  
; LENGTH: 15  
; TYPE: PPT  
; ORGANISM: Human Tyrosinase peptide  
US-09-036-582-22

Query Match 87.8%; Score 79; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFPPT 15  
| | | | | | | | | | | | | | |  
Db 1 QNILLSNAPLGQFPPT 15

RESULT 2  
US-09-183-706-25  
; Sequence 25, Application US/09183706  
; Patent No. 6245525  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/183,706  
; CURRENT FILING DATE: 1998-10-30  
; EARLIER APPLICATION NUMBER: 09/122,989  
; EARLIER FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 25  
; LENGTH: 15  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
US-09-183-706-25

Query Match 87.8%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
Db 1 QNILLSNAPLGQFPF 15

## RESULT 3

US-09-166-448-66  
; Sequence 66, Application US/09166448  
; Patent No. 6291430  
; GENERAL INFORMATION:  
; APPLICANT: Chau, Pascal  
; APPLICANT: Vantomme, Valrie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/09/166,448  
; CURRENT FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-166-448-66

Query Match 87.8%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
Db 1 QNILLSNAPLGQFPF 15

## RESULT 4

US-09-567-995-25  
; Sequence 25, Application US/09567995  
; Patent No. 6303756  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/567,995  
; CURRENT FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: 09/183,706  
; PRIOR FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-567-995-25

Query Match 87.8%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
Db 1 QNILLSNAPLGQFPF 15

## RESULT 5

US-09-165-863-22  
; Sequence 22, Application US/09165863  
; Patent No. 6407063  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Duffour, Marie-Therese  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Cornelis, Guy  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Lurquin, Christophe  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: Chau, Pascal  
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
; TITLE OF INVENTION: PROCEDURE  
; FILE REFERENCE: 11727  
; CURRENT APPLICATION NUMBER: US/09/165,863  
; CURRENT FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide  
US-09-165-863-22

Query Match 87.8%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15  
Db 1 QNILLSNAPLGQFPF 15

## RESULT 6

US-09-009-953-198  
; Sequence 198, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; REACTIVE DR RESTRICTED EPITOPES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,953  
; FILING DATE: 21-Jan-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,713  
; FILING DATE: 23-JAN-1997  
; APPLICATION NUMBER: US 60/037,432  
; FILING DATE: 07-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-011520US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; TELEX: <Unknown>

```
/ INFORMATION FOR SEQ ID NO: 198:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 15 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/   MOLECULE TYPE: peptide
/   SEQUENCE DESCRIPTION: SEQ ID NO: 198:
US-09-009-953-198

Query Match      87.8%; Score 79; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15
Db 1 QNILLSNAPLGQFPF 15

RESULT 7
US-09-697-884-66
/ Sequence 66, Application US/09697884
/ Patent No. 6426217
/ GENERAL INFORMATION:
/ APPLICANT: Chauv, Pascal
/ APPLICANT: Vantomme, Val.rie
/ APPLICANT: Stroobant, Vincent
/ APPLICANT: Boon-Falleur, Thierry
/ APPLICANT: van der Bruggen, Pierre
/ APPLICANT: Thielemans, Kris
/ APPLICANT: Corthals, Jurgen
/ TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
/ FILE REFERENCE: L0461/7052
/ CURRENT APPLICATION NUMBER: US/09/697,884
/ CURRENT FILING DATE: 2000-10-27
/ PRIOR APPLICATION NUMBER: 09/166,448
/ PRIOR FILING DATE: 1998-10-05
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 66
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-697-884-66

Query Match      87.8%; Score 79; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15
Db 1 QNILLSNAPLGQFPF 15

RESULT 8
US-09-289-350-22
/ Sequence 22, Application US/09289350
/ Patent No. 6531451
/ GENERAL INFORMATION:
/ APPLICANT: Chauv, Pascal
/ APPLICANT: Luiten, Rosalie
/ APPLICANT: Demotte, Nathalie
/ APPLICANT: Deffour, Marie-Therese
/ APPLICANT: Lurquin, Christophe
/ APPLICANT: Traversari, Catia
/ APPLICANT: Stroobant, Vincent
/ APPLICANT: Cornelis, Guy R.
/ APPLICANT: Boon-Falleur, Thierry
/ APPLICANT: Van Der Bruggen, Pierre
/ TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
/ FILE REFERENCE: 11727Z
/ CURRENT APPLICATION NUMBER: US/09/289,350

/ INFORMATION FOR SEQ ID NO: 199:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 15 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/   MOLECULE TYPE: peptide
/   SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-009-953-199

Query Match      87.8%; Score 79; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15
Db 1 QNILLSNAPLGQFPF 15

RESULT 9
US-09-574-749B-24
/ Sequence 24, Application US/09574749B
/ Patent No. 6548299
/ GENERAL INFORMATION:
/ APPLICANT: ROSENZWEIG, Michael
/ APPLICANT: PYKETT, Mark J.
/ APPLICANT: SCADDEN, David T.
/ APPLICANT: POZNANSKY, Mark C.
/ TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
/ TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
/ FILE REFERENCE: C1005/7012/KA/ERG
/ CURRENT APPLICATION NUMBER: US/09/574,749B
/ CURRENT FILING DATE: 2002-05-31
/ PRIOR APPLICATION NUMBER: US 60/107,972
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: PCT/US99/26795
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: US 09/524,749
/ PRIOR FILING DATE: 2000-05-18
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 24
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-24

Query Match      87.8%; Score 79; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFPF 15
Db 1 QNILLSNAPLGQFPF 15

RESULT 10
US-09-318-141-22
/ Sequence 22, Application US/09318141
/ Patent No. 6602506
/ GENERAL INFORMATION:
/ APPLICANT: van der Bruggen, Pierre
/ APPLICANT: Cornelis, Guy R.
/ TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
/ TITLE OF INVENTION: WITH RECOMBINANT YERSINIA
/ FILE REFERENCE: 11154
/ CURRENT APPLICATION NUMBER: US/09/318,141
/ CURRENT FILING DATE: 1999-05-25
/ EARLIER APPLICATION NUMBER: US 09/036,582
```

; EARLIER FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide  
US-09-318-141-22

Query Match 87.8%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

## RESULT 11

US-09-601-729-112  
; Sequence 112, Application US/09601729  
; Patent No. 6683052  
; GENERAL INFORMATION:  
; APPLICANT: THIAM, KADER  
; APPLICANT: AURIAULT, CLAUDE  
; APPLICANT: GRAS-MASSE, HELENE  
; APPLICANT: LOING, ESTELLE  
; APPLICANT: VERWAERDE, CLAUDIE  
; APPLICANT: GUILLET, JEAN GERARD  
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES  
; FILE REFERENCE: USB-97-AU-IN  
; CURRENT APPLICATION NUMBER: US/09/601,729  
; CURRENT FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: PCT/FR99/00259  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 98 01439  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 281  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 112  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-601-729-112

Query Match 87.8%; Score 79; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

## RESULT 12

US-09-169-717E-28  
; Sequence 28, Application US/09169717E  
; Patent No. 6667037  
; GENERAL INFORMATION:  
; APPLICANT: Ooms, Annie  
; APPLICANT: DeGiovanni, Gerard  
; APPLICANT: Morel, Sandra  
; APPLICANT: Van den Eynde, Benoit  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: Isolater Peptides Which Bind To HLA-B35 Molecules,  
; TITLE OF INVENTION: Larger Peptides Which Contain These, Nucleic Acid  
; FILE REFERENCE: LUB5561  
; CURRENT APPLICATION NUMBER: US/09/169,717E

; CURRENT FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 39  
; SEQ ID NO 28  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-169-717E-28

Query Match 80.0%; Score 72; DB 4; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.3e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQPP 15  
Db 1 QNILLSNAPLGQPP 15

## RESULT 13

US-08-902-516-41  
; Sequence 41, Application US/08902516  
; Patent No. 5891432  
; GENERAL INFORMATION:  
; APPLICANT: Soc Hoo, William  
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; TITLE OF INVENTION: RESPONSE USING SAME  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL & FLORES, LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,516  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IM 2442  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)535-9001  
; TELEFAX: (619)535-8949  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-902-516-41

Query Match 73.3%; Score 66; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQ 13  
Db 1 QNILLSNAPLGQ 13

## RESULT 14

US-09-847-185-41  
; Sequence 41, Application US/09847185  
; Patent No. 6482407  
; GENERAL INFORMATION:

```

;
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
;
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-9949
;
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-847-185-41

Query Match 73.3%; Score 66; DB 4; Length 13;
Best Local Similarity 100.0%; Pred.No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGPQ 13
Db 1 QNILLSNAPLGPQ 13

RESULT 15
US-08-159-339A-783
; Sequence 783, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 783:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-783

Query Match 36.7%; Score 33; DB 3; Length 9;
Best Local Similarity 85.7%; Pred.No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PLGPQFP 15
Db 2 PLGPQGP 8

Search completed: June 3, 2004, 15:27:52
Job time : 23 secs
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:24 ; Search time 13.5 Seconds  
(without alignments)  
106.879 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83  
Sequence: 1 DYSYLQSDPSFQD 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78.\*

1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	83	100.0	529	1 YRHU1	monophenol monooxy
2	54	65.1	533	1 YRMSCS	monophenol monooxy
3	49	59.0	336	1 A69416	pyruvate formate-1
4	45	54.2	274	2 JRM077	chitinase (EC 3.2.
5	45	54.2	393	2 AGL142	N-acyl-L-amino aci
6	45	54.2	393	2 AGL142	N-acyl-L-amino aci
7	45	54.2	476	2 C84687	probable fatty aci
8	43	51.8	150	2 T38629	hypothetical prote
9	43	51.8	620	2 S56790	probable membrane
10	43	51.8	1093	2 H84126	cation efflux syst
11	43	51.8	1744	2 JH0720	tanabin - African
12	42.5	51.2	862	2 JH0720	lipoxigenase (EC 1
13	41	49.4	517	2 F71417	cytochrome P450 -
14	41	49.4	561	2 D70034	oligo-1,6-glucosid
15	40	48.2	184	1 ZRPPT9	gene 3 protein - p
16	40	48.2	295	2 S29045	estrone sulfotrans
17	40	48.2	337	2 AK0972	lipopolysaccharide
18	40	48.2	368	2 T24974	hypothetical prote
19	40	48.2	550	1 HYSMCA	mycolysin (EC 3.4.
20	40	48.2	585	2 S06958	spingomyelin phos
21	40	48.2	596	2 S30973	minor tail protein
22	40	48.2	629	1 A39825	spingomyelin phos
23	40	48.2	638	2 A30347	exotoxin A precurs
24	40	48.2	638	2 C83503	exotoxin A precurs
25	40	48.2	901	2 C83427	probable transcrip
26	40	48.2	940	2 T01854	hypothetical prote
27	39	47.0	130	2 B82589	hypothetical prote
28	39	47.0	185	2 T15399	hypothetical prote
29	39	47.0	239	2 G37821	tRNA nucleotidyltr

## ALIGNMENTS

## RESULT 1

YRHU1

N:Alternate names: cressolase; monophenol oxidase; phenolase; tyrosinase

C:Species: Homo sapiens (man)

C&gt;Date: 30-Jun-1990 #sequence\_revision 31-Mar-1993 #text\_change 08-Dec-2000

C/Accession: A38444; S07760; A33393; A38718; JLM098; A40957; S04760; A60149; B60149; S53

R:Giebel, L.B.; Strunk, K.M.; Spritz, R.A.

Genomics 9, 435-445, 1991

A&gt;Title: Organization and nucleotide sequences of the human tyrosinase gene and a truncate

A/Reference number: A38444; MUID:91236163; PMID:1903356

A/Accession: A38444

A/Molecule type: DNA

A/Residues: 1-529 &lt;GIE&gt;

A/Cross-references: GB:M63239; GB:M60296; NID:G340033; PIDN:AAA61242.1; PID:G340035

R:Kikuchi, H.; Miura, H.; Yamamoto, H.; Takeuchi, T.; Dei, T.; Watanabe, M.

Biochim. Biophys. Acta 1009, 283-286, 1989

A&gt;Title: Characteristic sequences in the upstream region of the human tyrosinase gene.

A/Reference number: S07760; MUID:90089403; PMID:2490811

A/Accession: S07760

A/Molecule type: DNA

A/Residues: 1-273 &lt;KIT&gt;

A/Cross-references: EMBL:X16073; NID:G37506; PIDN:CAA34205.1; PID:G37507

R:Takeda, A.; Tomita, Y.; Okinaga, S.; Tagami, H.; Shibahara, S.

Biochem. Biophys. Res. Commun. 162, 984-990, 1989

A&gt;Title: Functional analysis of the cDNA encoding human tyrosinase precursor.

A/Reference number: A33393; MUID:89351001; PMID:2504160

A/Accession: A33393

A/Molecule type: DNA

A/Residues: 1-32 &lt;TAK&gt;

A/Cross-references: GB:M27160

R:Giebel, L.B.; Tripathi, R.K.; Strunk, K.M.; Hanifin, J.M.; Jackson, C.E.; King, R.A.;

Am. J. Hum. Genet. 48, 1159-1167, 1991

A&gt;Title: Tyrosinase gene mutations associated with type IB ("yellow") oculocutaneous alb

A/Reference number: A38718; MUID:91241133; PMID:1903551

A/Accession: A38718

A/Molecule type: DNA

A/Residues: 274-280; 401-411; 500-509 &lt;G12&gt;

R:Bouchard, B.; Fuller, B.B.; Vijayaradhi, S.; Houghton, A.N.

J. Exp. Med. 169, 2029-2042, 1989

A&gt;Title: Induction of pigmentation in mouse fibroblasts by expression of human tyrosinase

A/Reference number: JLM098

A/Accession: JLM098

A/Molecule type: mRNA

A/Residues: 'GR', 1-178, 'I', 180-191, 'V', 193-529 &lt;BOU&gt;

A/Cross-references: EMBL:Y00819; NID:G37508; PIDN:CAA68756.1; PID:G37509

R:Chintamaneni, C.D.; Halaban, R.; Kobayashi, Y.; Witkop Jr., C.J.; Kwon, B.S.

Proc. Natl. Acad. Sci. U.S.A. 88, 5272-5276, 1991

A&gt;Title: A single base insertion in the putative transmembrane domain of the tyrosinase

A/Reference number: A40957; MUID:91271371; PMID:1711223

A/Accession: A40957

A/Molecule type: mRNA

A;Residues: 1-165, 'I', 167-489, 'CPAGRACELAVSQEKAAS' <CHI>  
 A;Cross-references: GB:M74314  
 A;Experimental source: albino melanocytes  
 A;Note: Mutant protein isolated from patient with tyrosinase-negative oculocutaneous albinism  
 R;Kwon, B.S.; Haq, A.K.; Pomerantz, S.H.; Halaban, R.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 7473-7477, 1987  
 A;Title: Isolation and sequence of a cDNA clone for human tyrosinase that maps at the melanocyte locus  
 A;Reference number: A94185; MUID:88041128; PMID:2823263  
 A;Accession: S04760  
 A;Molecule type: mRNA  
 A;Residues: 1-241, 'TGV', 46-191, 'Y', 193-307, 'T', 309-372, 'HVPCT', 379-401, 'Q', 403-494, 'E'  
 A;Cross-references: GB:J03581; NID:G340027; PIDN:AAA61241.1; PID:G340028  
 A;Experimental source: normal melanocytes  
 A;Note: The sequence differs from that shown in several regions due to reading frameshift  
 R;Wittber, A.; Odh, G.; Rosengren, A.M.; Rosengren, E.; Rorsman, H.  
 Acta Derm. Venereol. 70, 291-294, 1990  
 A;Title: Isolation of soluble tyrosinase from human melanoma cells.  
 A;Reference number: A60149; MUID:91021767; PMID:1977251  
 A;Accession: A60149  
 A;Molecule type: protein  
 A;Residues: 19-23, 'X', 25-28 <WIT>  
 A;Note: the sequence was determined from a soluble form of the enzyme from melanoma cell  
 A;Accession: B60149  
 A;Molecule type: protein  
 A;Residues: 19-23, 'X', 25-34, 'XX', 37-38 <WIT>  
 A;Note: the sequence was determined from a membrane-bound form of the enzyme from melanoma cell  
 R;Glebel, L.B.; Strunk, K.M.; Spritz, R.A.  
 submitted to the EMBL Data Library, July 1991  
 A;Description: Organization and nucleotide sequences of the human tyrosinase gene and a cDNA  
 A;Reference number: S53560  
 A;Accession: S53560  
 A;Molecule type: DNA  
 A;Residues: 396-455 <G13>  
 A;Cross-references: EMBL:M63238  
 R;Wittber, A.; Dahlbaeck, B.; Odh, G.; Rosengren, A.M.; Rosengren, E.; Rorsman, H.  
 Acta Derm. Venereol. 69, 125-131, 1989  
 A;Title: Isolation of human tyrosinase from cultured melanoma cells.  
 A;Reference number: A60464; MUID:89163645; PMID:2564229  
 A;Accession: A60464  
 A;Molecule type: protein  
 A;Residues: 1-2-13, 13-23, 'X', 25-34, 'XX', 37-38 <W12>  
 R;Guo, Z.; Guilfoyle, R.A.; Thiel, A.J.; Wang, R.; Smith, L.M.  
 Nucleic Acids Res. 22, 5456-5465, 1994  
 A;Title: Direct fluorescence analysis of genetic polymorphisms by hybridization with oligonucleotide probes  
 A;Reference number: S53559; MUID:95116340; PMID:7816638  
 A;Contents: annotation  
 C;Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; it reacts in the formation of pigments such as melanins and other polyphenolic compounds  
 C;Genetics:  
 A;Gene: GDB:TYR  
 A;Cross-references: GDB:120476; OMIM:203100  
 A;Map position: 11q21-11q21  
 A;Introns: 273/3; 346/1; 395/2; 456/1  
 C;Superfamily: monophenol monooxygenase  
 C;Keywords: albinism; copper; glycoprotein; melanin biosynthesis; monooxygenase; oxidoreductase  
 F;1-19/Domain: signal sequence #status experimental <MAT>  
 F;19-529/Product: monophenol monooxygenase #status predicted <SIG>  
 F;474-500/Domain: transmembrane #status predicted <TM>  
 F;86,111,161,230,337,371/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F;180,202,211/Binding site: copper (His) #status predicted  
 F;363,367,390,420/Binding site: copper (His) #status predicted  
 Query Match 100.0%; Score 83; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPSFQD 15  
 DB 448 DYSYLQSDPSFQD 462  
 RESULT 2  
 YRMSCS

monophenol monooxygenase (EC 1.14.18.1) precursor [validated] - mouse  
 N;Alternate names: cresolase; monophenol oxidase; phenolase; tyrosinase  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 20-Apr-2000  
 C;Accession: A27711; A60778; A32429; B32429; S01170; S02278; S15753; I49736  
 R;Kwon, B.S.; Wakulchik, M.; Haq, A.K.; Halaban, R.; Kestler, D.  
 Biochem. Biophys. Res. Commun. 153, 1301-1309, 1988  
 A;Title: Sequence analysis of mouse tyrosinase cDNA and the effect of melanotropin on it  
 A;Reference number: A27711; MUID:88268910; PMID:3134020  
 A;Accession: A27711  
 A;Molecule type: mRNA  
 A;Residues: 1-533 <KWO>  
 A;Cross-references: GB:M20234; NID:G202247; PIDN:AAA40516.1; PID:G202248  
 A;Experimental source: Cloudman S-93 melanoma cells  
 R;Kwon, B.S.; Haq, A.K.; Wakulchik, M.; Kestler, D.; Barton, D.E.; Francke, U.; Lamoreux  
 J. Invest. Dermatol. 93, 589-594, 1989  
 A;Title: Isolation, chromosomal mapping, and expression of the mouse tyrosinase gene.  
 A;Reference number: A60778; MUID:90010220; PMID:2507645  
 A;Accession: A60778  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-273 <KWO>  
 A;Experimental source: BALB/c  
 R;Terao, M.; Tabe, L.; Garattini, E.; Sartori, D.; Studer, M.; Mintz, B.  
 Biochem. Biophys. Res. Commun. 159, 848-853, 1989  
 A;Title: Isolation and characterization of variant cDNAs encoding mouse tyrosinase.  
 A;Reference number: A32429; MUID:89193679; PMID:2494997  
 A;Accession: A32429  
 A;Molecule type: mRNA  
 A;Residues: 1-102, 'C', 104-345, 'G', 347-533 <TER>  
 A;Cross-references: GB:M24560; NID:G202249; PIDN:AAA40517.1; PID:G202250  
 A;Accession: B32429  
 A;Molecule type: mRNA  
 A;Residues: 1-77;155-345, 'G', 347-533 <TE2>  
 A;Cross-references: GB:M24560  
 A;Experimental source: B16 melanoma cells  
 R;Mueller, G.; Ruppert, S.; Schmid, E.; Schuetz, G.  
 EMBO J. 7, 2723-2730, 1988  
 A;Title: Functional analysis of alternatively spliced tyrosinase gene transcripts.  
 A;Reference number: S01170; MUID:89030636; PMID:3141148  
 A;Accession: S01170  
 A;Molecule type: mRNA  
 A;Residues: 1-102, 'C', 104-263, 'I', 265-345, 'G', 347-533 <MUE>  
 A;Cross-references: GB:X12782; NID:G55061; PIDN:CAA31273.1; PID:G55062  
 R;Yamamoto, H.; Takeuchi, S.; Kudo, T.; Makino, K.; Nakata, A.; Shinoda, T.; Takeuchi, T.  
 Jpn. J. Genet. 62, 271-274, 1987  
 A;Title: Cloning and sequencing of mouse tyrosinase cDNA.  
 A;Reference number: S02278  
 A;Accession: S02278  
 A;Molecule type: mRNA  
 A;Residues: 1-102, 'C', 104-263, 'I', 265-345, 'G', 347-448 <YAM>  
 A;Cross-references: EMBL:X12782  
 A;Note: part of this sequence was confirmed by protein sequencing  
 R;Shibahara, S.; Okinaga, S.; Tomita, Y.; Takeda, A.; Yamamoto, H.; Sato, M.; Takeuchi, T.  
 Eur. J. Biochem. 189, 455-461, 1990  
 A;Title: A point mutation in the tyrosinase gene of BALB/c albino mouse causing the cyst  
 A;Reference number: S15753; MUID:90249393; PMID:2110899  
 A;Accession: S15753  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-13 <SHI>  
 A;Cross-references: EMBL:X51743; NID:G55057; PIDN:CAA36033.1; PID:G55058  
 A;Experimental source: strain BALB/c  
 R;Kwon, B.S.; Halaban, R.; Chintamani, C.  
 Biochem. Biophys. Res. Commun. 161, 252-260, 1989  
 A;Title: Molecular basis of mouse Himalayan mutation.  
 A;Reference number: I49736; MUID:89273644; PMID:2567165  
 A;Accession: I49736  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-39, 'I', 41-102, 'C', 104-196, 'Q', 198-345, 'G', 347-419, 'R', 421-533 <RES>  
 A;Cross-references: GB:M26729; NID:G193845; PIDN:AAA37806.1; PID:G309296  
 C;Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; it

reactions in the formation of pigments such as melanins and other polyphenolic compound

C:Genetics:  
A:Gene: Tyr1  
A:Map position: 7  
C:Superfamily: monophenol monooxygenase  
C:Keywords: albinism; alternative splicing; copper; glycoprotein; melanin biosynthesis;  
R:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-533/Product: monophenol monooxygenase #status predicted <MAT>  
F:474-497/Domain: transmembrane #status predicted <TM>  
F:86,111,161,230,337,371/Binding site: carbonylrate (Asn) (covalent) #status predicted

Query Match 65.1%; Score 54; DB 1; Length 533;  
Best Local Similarity 60.0%; Pred. No. 0.66;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYSYLQSDSPDPSFQD 15  
DB 448 DYSYLQSDSPDPSFQD 462

RESULT 3  
A69416  
pyruvate formate-lyase activating enzyme (act-3) homolog - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: A69416  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
R: Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A:Reference number: A69250; MUID:98049343; PMID:9389475  
A:Accession: A69416  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-336 <KLE>  
A:Cross-references: GB:AE001012; GB:AE000782; NID:G2689335; PIDN:AAB89917.1; PID:G264924  
C:Superfamily: conserved hypothetical protein MJ0808

Query Match 59.0%; Score 49; DB 1; Length 336;  
Best Local Similarity 66.7%; Pred. No. 2.5;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYLQSDSPDPS 12  
DB 100 DYSYLREIDPDT 111

RESULT 4  
JW0077  
chitinase (EC 3.2.1.14) a - Gladiolus gandavensis  
C:Species: Gladiolus gandavensis  
C:Date: 17-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 07-May-1999  
C:Accession: JW0077  
R: Yamagami, T.; Mine, Y.; Ishiguro, M.  
Biochem. Biotechnol. Biochem. 62, 386-389, 1998  
A:Title: Complete amino acid sequence of chitinase-a from bulbs of gladiolus (Gladiolus  
A:Reference number: JW0077; MUID:98193995; PMID:9532802  
A:Accession: JW0077  
A:Molecule type: protein  
A:Residues: 1-274 <YAM>  
A:Experimental source: bulbs  
C:Comment: This enzyme hydrolyzes beta-1,4-linked N-acetylglucosamine polymer chitin.  
C:Superfamily: alcohol sulfotransferase  
C:Keywords: glycosidase; hydrolase

Query Match 54.2%; Score 45; DB 2; Length 274;  
Best Local Similarity 46.7%; Pred. No. 9;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DYSYLQSDSPDPSFQD 15

Db 124 DYENFQTDPTFAE 138  
|||::|||::|

RESULT 5  
AC1142  
N-acyl-L-amino acid amidohydrolase homolog lmo0538 [imported] - Listeria monocytogenes  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AC1142  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
Science 294, 849-852, 2001  
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AC1142  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-393 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAC98617.1; PID:gl6409914; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0538  
C:Superfamily: hippurate hydrolase

Query Match 54.2%; Score 45; DB 2; Length 393;  
Best Local Similarity 61.5%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DYSYLQSDSPDPSF 13  
DB 333 DYSYFQDEAPGSF 345  
|||::|||::|

RESULT 6  
AF1500  
N-acyl-L-amino acid amidohydrolase homolog lin0542 [imported] - Listeria innocua (strain  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AF1500  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kref, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AF1500  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-393 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC95774.1; PID:gl6412982; GSPDB:GN00178  
A:Experimental source: strain Clp11262  
C:Genetics:  
A:Gene: lin0542  
C:Superfamily: hippurate hydrolase

Query Match 54.2%; Score 45; DB 2; Length 393;  
Best Local Similarity 61.5%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DYSYLQSDSPDPSF 13  
DB 333 DYSYFQDEAPGSF 345  
|||::|||::|

RESULT 7  
CB4687  
probable fatty acid elongase [imported] - Arabidopsis thaliana



R;Veronesi, C.; Fournier, J.; Rickauer, M.; Esquerre-Tugaye, M.T.  
submitted to the EMBL Data Library, January 1995  
A;Description: Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA.  
A;Reference number: S57964  
A;Accession: S57964  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-862 <VER>  
A;Cross-references: EMBL:X84040; NID:g899343; PIDN:CAA58859.1; PID:g899344  
C;Superfamily: lipoxigenase  
C;Keywords: oxidoreductase

Query Match 51.2%; Score 42.5; DB 2; Length 862;  
Best Local Similarity 56.2%; Pred. No. 84;  
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 1 DYSYLQSDPDSPQD 15  
|||:|:|:|:|:|:|  
Db 200 DYAYNDLGDPPKQGD 215  
|||:|:|:|:|:|:|

RESULT 13  
F71417  
Cytochrome P450 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
A;Variety: Columbia  
C;Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 20-Jun-2000  
C;Accession: F71417  
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk  
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel  
avannah, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
Nature 391, 485-488, 1998  
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech  
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ana  
C.; Chalwatzis, N.  
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal  
A;Reference number: A71400; MUID:98121113; PMID:9461215  
A;Accession: F71417  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-517 <BEV>  
A;Cross-references: GB:297338; NID:g2244870; PIDN:CAB10312.1; PID:g2244891  
C;Genetics:  
A;Map position: 4COP9-4G3845  
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
C;Keywords: chromoprotein; heme; iron; metalloprotein  
F:308-474/Domain: cytochrome P450 homology <P45>  
F:452/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 49.4%; Score 41; DB 2; Length 517;  
Best Local Similarity 61.5%; Pred. No. 82;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 SYLQSDPDSPQD 15  
|||:|:|:|:|:|:|  
Db 404 SYAMMRDPDSQD 416  
|||:|:|:|:|:|:|

RESULT 14  
D70034  
oligo-1,6-glucosidase homolog yvdL - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C;Accession: D70034  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, I  
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: D70034  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-561 <KUN>  
A;Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CAB15461.1; PID:g2635969  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: yvdL  
C;Superfamily: alpha-glucosidase; alpha-amylase core homology  
F:167-335/Domain: alpha-amylase core homology <AMY>

Query Match 49.4%; Score 41; DB 2; Length 561;  
Best Local Similarity 53.8%; Pred. No. 90;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDSPF 13  
|||:|:|:|:|:|:|  
Db 484 DYQLQENDPQVF 496  
|||:|:|:|:|:|:|

RESULT 15  
ZRBPT9  
gene 3 protein - phage T4  
C;Species: phage T4  
A;Note: host Escherichia coli  
C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 23-Jul-1999  
C;Accession: C32254; S04611  
R;Lipinska, B.; Rao, A.S.M.K.; Bolten, B.M.; Balakrishnan, R.; Goldberg, E.B.  
J. Bacteriol. 171, 498-497, 1989  
A;Title: Cloning and identification of bacteriophage T4 gene 2 product gp2 and action of  
A;Reference number: A91899; MUID:89123061; PMID:2644202  
A;Accession: C32254  
A;Molecule type: DNA  
A;Residues: 1-184 <LIP>  
A;Cross-references: GB:M23012; NID:g340786; PIDN:AAA50419.1; PID:g557583  
R;Koch, T.; Lamm, N.; Rueger, W.  
Nucleic Acids Res. 17, 4392, 1989  
A;Title: Sequencing, cloning and overexpression of genes of bacteriophage T4 between map  
A;Reference number: S04508; MUID:89296504; PMID:2740234  
A;Accession: S04611  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-176 <KOC>  
A;Cross-references: EMBL:X14845; NID:g15218; PIDN:CAA32952.1; PID:g15222  
C;Genetics:  
A;Gene: 3  
C;Superfamily: phage T4 gene 3 protein

Query Match 48.2%; Score 40; DB 1; Length 184;  
Best Local Similarity 60.0%; Pred. No. 37;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYSYLQSDP 10  
:|:|:|:|:|:|  
Db 142 EFSYTEDSDP 151  
:|:|:|:|:|:|

Search completed: June 3, 2004, 15:15:26  
Job time : 14.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:24 ; Search time 10 Seconds  
(without alignments)  
78.105 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DYSYLQSDPSDFQD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	83	100.0	529	1 TYRO HUMAN	P14679 homo sapien
2	54	65.1	533	1 TYRO MOUSE	P11344 mus musculus
3	45	54.2	337	1 RFAI SALT	P19816 salmonella
4	45	54.2	529	1 TYRO CHICK	P55024 gallus gall
5	43	51.8	457	1 ERFI GIALA	Q9ncp1 giardia lam
6	43	51.8	497	1 G6PI LSGPN	Q9rdy2 legionella
7	43	51.8	620	1 XJB9 YEAST	P47069 saccharomyc
8	43	51.8	1744	1 TANA XENLA	Q01550 xenopus lae
9	41	49.4	561	1 O16G BACSU	O06994 bacillus eu
10	40.5	48.8	264	1 SNAI HUMAN	Q95863 homo sapien
11	40	48.2	176	1 VG03 BPT4	P13331 bacterioph
12	40	48.2	295	1 SUOE BOVIN	P19217 bos taurus
13	40	48.2	550	1 MYCO STRECI	P20910 streptomyce
14	40	48.2	595	1 VG28 BPMU5	Q05235 mycobacteri
15	40	48.2	629	1 ASM HUMAN	P17405 homo sapien
16	40	48.2	638	1 TOXA PSEAE	P11439 pseudomonas
17	39	47.0	215	1 KCY STREP	Q8csh5 staphylococ
18	39	47.0	239	1 RNPH RICCN	Q92927 rickettsia
19	39	47.0	322	1 Y711 METUA	Q58121 methanococc
20	39	47.0	548	1 AAKI RAT	P54645 rattus norv
21	39	47.0	550	1 AAKI HUMAN	Q13131 homo sapien
22	39	47.0	564	1 ASMI CABEL	P17405 caenorhabdi
23	39	47.0	588	1 HUTU HALNI	Q9hqd8 halobacteri
24	39	47.0	779	1 YU20 ARATH	Q9zpv5 arabidopsis
25	39	47.0	1129	1 EG27 CABEL	Q09228 caenorhabdi
26	39	47.0	1235	1 KPB2 MOUSE	Q8bwj3 mus musculus
27	39	47.0	1486	1 MUXE ECOLI	P22523 escherichia
28	38.5	46.4	399	1 WR48 ARATH	Q9fgz4 arabidopsis
29	38	45.8	242	1 GLUA COREF	Q8rq17 corynebacte
30	38	45.8	268	1 COQA DROME	Q9vrg6 xenophila
31	38	45.8	402	1 LHX5 XENLA	F37137 xenopus lae
32	38	45.8	412	1 GLYA METAC	Q8tk94 methanosaer
33	38	45.8	475	1 PRTG ERWCH	Q07162 erwinia chr

## RESULT 1

34	38	45.8	502	1 TBG CANAL	O93807 candida alb
35	38	45.8	520	1 CCB4 HUMAN	O00305 homo sapien
36	38	45.8	540	1 Y99A_RHOBA	Q7ukt5 rhodospirill
37	38	45.8	595	1 VG28_BPMU2	O64222 mycobacteri
38	38	45.8	603	1 LCB2_SCHPO	O09925 schizosacch
39	38	45.8	649	1 FAF1_MOUSE	P54731 mus musculus
40	38	45.8	650	1 FAF1_HUMAN	Q9unn5 homo sapien
41	38	45.8	660	1 ALIA_STREN	P35592 streptococc
42	38	45.8	694	1 CMG3_HUMAN	Q16281 homo sapien
43	38	45.8	1237	1 YG2L_YEAST	P53254 saccharomyc
44	38	45.8	1365	1 GTFS_STRDO	P29336 streptococc
45	37	44.6	188	1 GIDB_CAWJE	Q9pnu3 campylobact

## ALIGNMENTS

AC	TYRO HUMAN	STANDARD;	PRT;	529 AA.
DT	01-APR-1990	(Rel. 14, Created)		
DT	01-JUL-1993	(Rel. 26, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)			
DE	(Tumor rejection antigen AB) (SK29-AB) (LB24-AB).			
GN	TYR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=91236163; PubMed=1903356;			
RA	Giebel L.B., Strunk K.M., Spritz R.A.;			
RT	"Organization and nucleotide sequences of the human tyrosinase gene			
RT	and a truncated tyrosinase-related segment.";			
RL	Genomics 9:435-445(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=88041128; PubMed=2823263;			
RA	Kwon B.S., Haq A.K., Pomerantz S.H., Halaban R.;			
RT	"Isolation and sequence of a cDNA clone for human tyrosinase that			
RT	maps at the mouse C-albino locus.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7473-7477(1987).			
RN	[3]			
RP	REVISIONS TO 384-398.			
RA	Kwon B.S., Haq A.K., Pomerantz S.H., Halaban R.;			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:6352-6352(1988).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Melanoma;			
RX	MEDLINE=89279151; PubMed=2499655;			
RA	Bouchard B., Fuller B.B., Vijayaradhi S., Houghton A.N.;			
RT	"Induction of pigmentation in mouse fibroblasts by expression of			
RT	human tyrosinase cDNA.";			
RL	J. Exp. Med. 169:2029-2042(1989).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=91271371; PubMed=1711223;			
RA	Chintaneni C.D., Halaban R., Kobayashi Y., Witkop C.J., Kwon B.S.;			
RT	"A single base insertion in the putative transmembrane domain of the			
RT	tyrosinase gene as a cause for tyrosinase-negative oculocutaneous			
RT	albinism.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5272-5276(1991).			
RN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Melanoma, and T-cell;			
RA	Medline=93340625; PubMed=8340755;			
RX	Brichard V., van Pel A., Woelfel T., Woelfel C., de Plaen E.,			
RA	Lethe B., Coulie P., Boon T.;			
RT	"The tyrosinase gene codes for an antigen recognized by autologous			
RT	cytolytic T lymphocytes on HLA-A2 melanomas.";			

RL J. Exp. Med. 178:489-495(1993).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT TYR-192.  
RX MEDLINE=21026558; PubMed=11153699;  
RA Martinez-Arias R., Conas D., Andres A., Abello M.T., Domingo-Roura X.,  
RA Berranpetit J.;  
RT "The tyrosinase gene in gorillas and the albinism of 'Snowflake'";  
RL Pigment Cell Res. 13:467-470(2000).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE OF 1-272 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=90089403; PubMed=2480811;  
RA Kikuchi H., Miura H., Yamamoto H., Takeuchi T., Dei T., Watanabe M.;  
RT "Characteristic sequences in the upstream region of the human  
RT tyrosinase gene";  
RL Biochim. Biophys. Acta 1009:283-286(1989).  
RN [10]  
RP SEQUENCE OF 1-32 FROM N.A.  
RX MEDLINE=89351001; PubMed=2504160;  
RA Takeda A., Tomita Y., Okinaga S., Tagami H., Shibahara S.;  
RT "Functional analysis of the cDNA encoding human tyrosinase  
RT precursor";  
RL Biochem. Biophys. Res. Commun. 162:984-990(1989).  
RN [11]  
RP SEQUENCE OF 54-195 FROM N.A., AND VARIANT TYR-192.  
RX MEDLINE=21082082; PubMed=11214319;  
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RA O'Brien S.J.;  
RT "Molecular phylogenetics and the origins of placental mammals";  
RL Nature 409:614-618(2001).  
RN [12]  
RP REVIEW ON OCA VARIANTS.  
RX MEDLINE=93237884; PubMed=8477259;  
RA Oetting W.S., King R.A.;  
RT "Molecular basis of type I (tyrosinase-related) oculocutaneous  
RT albinism: mutations and polymorphisms of the human tyrosinase gene";  
RL Hum. Mutat. 2:1-6(1993).  
RN [13]  
RP REVIEW ON OCA-I VARIANTS.  
RX MEDLINE=99140254; PubMed=10094567;  
RA Oetting W.S., King R.A.;  
RT "Molecular basis of albinism: mutations and polymorphisms of  
RT pigmentation genes associated with albinism";  
RL Hum. Mutat. 13:99-115(1999).  
RN [14]  
RP VARIANTS TYR-192; GLN-402; OCA-IA LYS-373 AND OCA-IA ASN-383.  
RX MEDLINE=90259036; PubMed=2342539;  
RA Spritz R.A., Strunk K.M., Giebel L.B., King R.A.;  
RT "Detection of mutations in the tyrosinase gene in a patient with type  
IA oculocutaneous albinism";  
RL New Engl. J. Med. 322:1724-1728(1990).  
RN [15]  
RP VARIANT OCA-IA LEU-81.  
RX MEDLINE=90238592; PubMed=1970634;  
RA Giebel L.B., Strunk K.M., King R.A., Hanifin J.M., Spritz R.A.;  
RT "A frequent tyrosinase gene mutation in classic, tyrosinase-negative  
RT (type IA) oculocutaneous albinism";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:3255-3258(1990).  
RN [16]  
RP VARIANTS OCA-IB PHE-275 AND LEU-406.  
RX MEDLINE=91241133; PubMed=1903591;  
RA Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,  
RA King R.A., Spritz R.A.;  
RT "Tyrosinase gene mutations associated with type IB ('yellow')  
RT oculocutaneous albinism";  
RL Am. J. Hum. Genet. 48:1159-1167(1991).  
RN [17]  
RP ERRATUM.  
RA Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,  
RA King R.A., Spritz R.A.;  
RL Am. J. Hum. Genet. 49:696-696(1991).  
RN [18]  
RP VARIANTS OCA-IA SER-21; TRP-217; HIS-299; SER-403; SER-446 AND  
RP ASN-448.  
RX MEDLINE=92351982; PubMed=1642278;  
RA Tripathi R.K., Strunk K.M., Giebel L.B., Weleber R.G., Spritz R.A.;  
RT "Tyrosinase gene mutations in type I (tyrosinase-deficient)  
RT oculocutaneous albinism define two clusters of missense  
RT substitutions";  
RL Am. J. Med. Genet. 43:865-871(1992).  
RN [19]  
RP VARIANT OCA-IA ARG-89.  
RX MEDLINE=91118940; PubMed=1899321;  
RA Spritz R.A., Strunk K.M., Heieh C.-L., Sekhon G.S., Francke U.;  
RT "Homozygous tyrosinase gene mutation in an American black with  
RT oculocutaneous albinism. A human homologue to the Siamese cat and the  
RT Himalayan mouse";  
RL Am. J. Hum. Genet. 48:318-324(1991).  
RN [20]  
RP VARIANT OCA-ITS GLN-422.  
RX MEDLINE=91154384; PubMed=1900309;  
RA Giebel L.B., Tripathi R.K., King R.A., Spritz R.A.;  
RT "A tyrosinase gene missense mutation in temperature-sensitive type I  
RT oculocutaneous albinism. A human homologue to the Siamese cat and the  
RT Himalayan mouse";  
RL J. Clin. Invest. 87:1119-1122(1991).  
RN [21]  
RP VARIANTS OCA-IA GLY-42; TYR-55; THR-206 AND ARG-419.  
RX MEDLINE=92048465; PubMed=1943686;  
RA King R.A., Mentink M.M., Oetting W.S.;  
RT "Non-random distribution of missense mutations within the human  
RT tyrosinase gene in type I (tyrosinase-related) oculocutaneous  
RT albinism";  
RL Mol. Biol. Med. 8:19-29(1991).  
RN [22]  
RP VARIANTS OCA-IA ILE-176 AND GLN-217.  
RX MEDLINE=93138611; PubMed=1487241;  
RA Oetting W.S., King R.A.;  
RT "Molecular analysis of type I-A (tyrosinase negative) oculocutaneous  
RT albinism";  
RL Hum. Genet. 90:258-262(1992).  
RN [23]  
RP VARIANTS OCA-IA GLN-328; ARG-419 AND LEU-431.  
RX MEDLINE=94070862; PubMed=7902671;  
RA Tripathi R.K., Bunday S., Musarella M.A., Droetto S., Strunk K.M.,  
RA Holmes S.A., Spritz R.A.;  
RT "Mutations of the tyrosinase gene in Indo-Pakistani patients with type  
RT I (tyrosinase-deficient) oculocutaneous albinism (OCA)";  
RL Am. J. Hum. Genet. 53:1173-1179(1993).  
RN [24]  
RP VARIANTS OCA-IA ASP-47; CYS-217 DEL; HIS-299 AND LYS-373, AND VARIANTS  
RP OCA-IB SER-152 AND LYS-294.  
RX MEDLINE=94175072; PubMed=8128955;

Query Match 100.0%; Score 83; DB 1; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1.le-05;  
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DYSYLQSDPSDFQD 15  
DB 448 DYSYLQSDPSDFQD 462

## RESULT 2

ID TYRO MOUSE STANDARD; PRT; 533 AA.  
AC P11344;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)  
DE (Albino locus protein).  
GN TYR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DBA/2J;  
RX MEDLINE=88268910; PubMed=3134020;  
RA Kwon B.S., Wakulchik M., Haq A.K., Halaban R., Kestler D.;  
RT "Sequence analysis of mouse tyrosinase cDNA and the effect of melanotropin on its gene expression."  
RL Biochem. Biophys. Res. Commun. 153:1301-1309 (1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Himalayan;  
RX MEDLINE=89273644; PubMed=2567165;  
RA Kwon B.S., Halaban R., Chintamaneni C.;  
RT "Molecular basis of mouse Himalayan mutation."  
RL Biochem. Biophys. Res. Commun. 161:252-260 (1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89030636; PubMed=3141148;  
RA Mueller G., Ruppert S., Schmid E., Schuetz G.;  
RT "Functional analysis of alternatively spliced tyrosinase gene transcripts."  
RL EMBO J. 7:2723-2730 (1988).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89193679; PubMed=2494997;  
RA Terao M., Tabé L., Garattini E., Sartori D., Studer M., Mintz B.;  
RT "Isolation and characterization of variant cDNAs encoding mouse tyrosinase."  
RL Biochem. Biophys. Res. Commun. 159:848-853 (1989).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Yamamoto H., Takeuchi S., Kudo T., Makino K., Nakata A., Shinoda T., Takeuchi T.;  
RT "Cloning and sequencing of mouse tyrosinase cDNA."  
RL Jpn. J. Genet. 62:271-274 (1987).  
RN [6]  
RP SEQUENCE OF 1-273 FROM N.A.  
RX MEDLINE=90212084; PubMed=2517217;  
RA Yamamoto H., Takeuchi S., Kudo T., Sato C., Takeuchi T.;  
RT "Melanin production in cultured albino melanocytes transfected with mouse tyrosinase cDNA."  
RL Jpn. J. Genet. 64:121-135 (1989).  
RN [7]  
RP VARIANT ALBINO.  
RC STRAIN=BALB/c;  
RX MEDLINE=90249393; PubMed=2110899;  
RA Shibahara S., Okinaga S., Tomita Y., Takeda A., Yamamoto H., Sato M., Takeuchi T.;  
RT "A point mutation in the tyrosinase gene of BALB/c albino mouse causing the cysteine->serine substitution at position 85.";  
Eur. J. Biochem. 189:455-461 (1990).  
RN [8]  
RP VARIANT CHINCHILLA MICE.  
RX MEDLINE=90360993; PubMed=2118105;  
RA Beermann F., Ruppert S., Hummler E., Bosch F.X., Mueller G., Ruether U., Schuetz G.;  
RT "Rescue of the albino phenotype by introduction of a functional tyrosinase gene into mice."  
RL EMBO J. 9:2819-2826 (1990).  
CC -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO INDOLE-5,6 QUINONE.  
CC -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA + DOPAquinone + H(2)O.  
CC -!- COFACTOR: Binds 2 copper ions per subunit.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.  
CC -!- DISEASE: DEFECTS IN TYR RESULT IN VARIOUS FORMS OF ALBINISM. HIMALAYAN STRAIN TYROSINASE IS TEMPERATURE-SENSITIVE.  
CC -!- SIMILARITY: Belongs to the tyrosinase family.  
CC -!- CAUTION: REF.4 SEQUENCE WAS INCORRECT DUE TO A DELETION OF EXON 3.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
EMBL; D00440; BAA00341.1; -  
EMBL; M20234; AAA40516.1; -  
EMBL; M26729; AAA37806.1; -  
EMBL; X12782; CAA31273.1; -  
EMBL; M24560; AAA40517.1; -  
EMBL; D00131; BAA00079.1; -  
EMBL; X51743; CAA36033.1; -  
EMBL; D00439; BAA00340.1; -  
PIR; A27711; YRMSCS.  
MGD; MGI:98880; Tyr.  
InterPro; IPR008922; Di-copper\_centre.  
InterPro; IPR002227; Tyrosinase.  
Pfam; PF00264; tyrosinase; 1.  
PRINTS; PR00092; TYROSINASE.  
PROSITE; PS00497; TYROSINASE\_1; 1.  
PROSITE; PS00498; TYROSINASE\_2; 1.  
Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;  
Transmembrane; Melanin biosynthesis; Disease mutation; Albinism.  
SIGNAL 1 18  
CHAIN 19 533 TYROSINASE.  
DOMAIN 19 476 LUMENAL, MELANOSOME (POTENTIAL).  
DOMAIN 477 497 POTENTIAL.  
DOMAIN 498 533 CYTOPLASMIC (POTENTIAL).  
METAL 180 180 COPPER A (BY SIMILARITY).  
METAL 202 202 COPPER A (BY SIMILARITY).  
METAL 211 211 COPPER A (BY SIMILARITY).  
METAL 363 363 COPPER B (BY SIMILARITY).  
METAL 367 367 COPPER B (BY SIMILARITY).  
METAL 390 390 COPPER B (BY SIMILARITY).  
DOMAIN 503 508 POLY-LYS.  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 111 111 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 337 337 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARIANT 103 103 C -> S (IN ALBINO MICE).  
FT VARIANT 420 420 H -> R (IN HIMALAYAN STRAIN).  
FT VARIANT 482 482 A -> T (IN CHINCHILLA MICE).  
FT VARIANT 482 482 M -> I (IN REF. 2).  
FT CONFLICT 40 40





between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-ch.ch](mailto:license@sib-ch.ch).

EMBL; D88349; BAAL3590.1; -.  
EMBL; L46805; AAB08441.1; -.  
PIR; PC4153; PC4153.  
InterPro; IPR008922; Di-copper centre.  
InterPro; IPR002227; Tyrosinase.  
Pfam; PF00264; tyrosinase\_1.  
PRINTS; PR00092; TYROSINASE.  
PROSITE; PS00497; TYROSINASE\_1; 1.  
PROSITE; PS00498; TYROSINASE\_2; 1.  
Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;  
Transmembrane; Melanin biosynthesis.  
SIGNAL 1 18  
CHAIN 19 529 TYROSINASE.  
DOMAIN 19 476 LUMENAL, MELANOSOME (POTENTIAL).  
TRANSMEM 477 497 POTENTIAL.  
DOMAIN 498 529 CYTOPLASMIC (POTENTIAL).  
METAL 180 180 COPPER A (BY SIMILARITY).  
METAL 202 202 COPPER A (BY SIMILARITY).  
METAL 211 211 COPPER A (BY SIMILARITY).  
METAL 363 363 COPPER B (BY SIMILARITY).  
METAL 367 367 COPPER B (BY SIMILARITY).  
METAL 390 390 COPPER B (BY SIMILARITY).  
CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 111 111 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 327 327 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).  
SEQUENCE 529 AA; 60357 MW; 74846452C3EFFB5 CRC64;

Query Match 54.2%; Score 45; DB 1; Length 529;  
 Local Similarity 60.0%; Pred. No. 12;  
 Conserved 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

1 DYSYLQDSPPDSFQD 15  
|||: |||  
448 DYEYLQEPALGSFQD 462

T 5

GIALA	
ERF1 GIALA	STANDARD;
	PRT; 457 AA.
Q9NCP1;	
16-OCT-2001	(Rel. 40, Created)
16-OCT-2001	(Rel. 40, last sequence update)
16-OCT-2001	(Rel. 40, last annotation update)
Eukaryotic peptide chain release factor subunit 1 (eRF1) (Eukaryotic release factor 1).	
ERF1.	

Giardia lamblia (Giardia intestinalis).  
Eukaryota; Diplomonadida; Hexamitidae; Giardia.  
NCBI\_TaxID=5741;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=20293306; PubMed=10833194;  
Inagaki Y., Doolittle W.F.;  
"Evolution of the eukaryotic translation termination system: origins  
of release factors.";  
Mol. Biol. Evol. 17:882-889(2000).  
-!- FUNCTION: Directs the termination of nascent peptide synthesis  
(translation) in response to the termination codons UAA, UAG and  
UGA (By similarity).  
-!- SUBUNIT: Heterodimer of two subunits, one of which binds GTP.  
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

```

DR PFAM: PF00342; PGI: 1.
DR PRINTS: PR00562; G6PISOMERASE
DR PROSITE: PS00765; P-GLUCOSE ISOMERASE 1; 1.
DR PROSITE: PS00174; P-GLUCOSE ISOMERASE 2; 1.
KW Isomerase; Gluconeogenesis; Glycolysis.
FT ACT SITE 381 BY SIMILARITY.
FT ACT SITE 485 BY SIMILARITY.
SQ SEQUENCE 497 AA; 56091 MW; 8CDA94027718310C CRC64;

Query Match 51.8%; Score 43; DB 1; Length 497;
Best Local Similarity 46.7%; Pred. No. 23;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DYSYLQSDSPDSFQD 15
DB 180 NHFISVDVPASFD 194

RESULT 7
XJB9 YEAST
ID _XJB9 YEAST STANDARD; PRT; 620 AA.
AC P47069;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 72.4 kDa protein in PET130-CT3 intergenic region.
GN YJL019W OR J1310.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA To Van D., Perea J., Jacq C.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z49294; CAA89309.1; -
DR PIR: S56790; S56790.
DR GO: S0003556; YJL019W.
DR GO: GO:0016021; C:integral to membrane; IDA.
DR GO: GO:0000743; P:nuclear migration during conjugation with c. . .; IMP.
DR GO: GO:0007103; P:spindle pole body duplication (sensu Saccha. . .; IMP.
KW Hypothetical protein; Transmembrane; ATP-binding.
FT DOMAIN 88 93 POLY-ASP.
FT TRANSMEM 155 175 POTENTIAL.
FT NP BIND 187 194 ATP (POTENTIAL).
FT DOMAIN 391 401 POLY-GLN.
SQ SEQUENCE 620 AA; 72385 MW; 18EC13469B9A5C6B CRC64;

Query Match 51.8%; Score 43; DB 1; Length 620;
Best Local Similarity 53.8%; Pred. No. 30;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYSYLQSDSPDSF 13
DB 116 DKSFIEDSDSY 128

RESULT 8
TANA_XENLA
ID TANA_XENLA STANDARD; PRT; 1744 AA.
AC Q01550;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

```

---

```

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Tanabin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tadpole head.
RX MEDLINE=92398961; Pubmed=1524825;
RA Hemmati-Briavaniou A., Mann R.W., Harland R.M.;
RT "A protein expressed in the growth cones of embryonic vertebrate
RT neurons defines a new class of intermediate filament protein.";
RL Neuron 9:417-428(1992)
CC -1- TISSUE SPECIFICITY: GROWTH CONES OF EMBRYONIC VERTEBRATE NEURONS.
CC -1- DEVELOPMENTAL STAGE: IS EXPRESSED IN THE NEURULA AND PERSIST
CC DURING EMBRYOGENESIS IN THE BRAIN, CRANIAL NERVES, AND SPINAL
CC CORD.
CC -1- SIMILARITY: Belongs to the intermediate filament family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M99387; AAA49966.1; -
DR PIR: JH0720; JH0720.
DR InterPro: IPR001664; IF.
DR Pfam: PF00038; filament; 1.
DR PROSITE: PS00225; IF; 1.
KW Intermediate filament; Coiled coil; Neurone.
FT DOMAIN 1 12 HEAD.
FT DOMAIN 13 314 ROD.
FT DOMAIN 315 1744 TAIL.
FT DOMAIN 8 48 COIL 1A.
FT DOMAIN 49 60 LINKER 1.
FT DOMAIN 61 156 COIL 1B.
FT DOMAIN 157 179 LINKER 12.
FT DOMAIN 180 193 COIL 2A.
FT DOMAIN 194 199 LINKER 2.
FT DOMAIN 200 314 COIL 2B.
SQ SEQUENCE 1744 AA; 199561 MW; 6502EAC9FE6C4E93 CRC64;

Query Match 51.8%; Score 43; DB 1; Length 1744;
Best Local Similarity 53.3%; Pred. No. 96;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DYSYLQSDSPDSFQD 15
DB 941 EVDYLQNYDEDSFQ 955

RESULT 9
O16G_BACSU
ID O16G_BACSU STANDARD; PRT; 561 AA.
AC O06994;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Oligo-1,6-glucosidase (EC 3.2.1.10) (Oligosaccharide alpha-1,6-
DE glucosidase) (Sucrase-isomaltase) (Isomaltase)
DE glucanohydrolase).
GN MALL OR BSU34560.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;

```

RA Denizot F.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377;  
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bertero M.G., Besieres P., Bolotin A., Borchert S.,  
RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Broutlet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
RA Entian K.D., Errington J., Fabret C., Fekari E., Foulger D.,  
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,  
RA Guisepi G., Guy B.J., Haga K., Haeht J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hoshono S., Hullo M.F., Itaya M., Jones L.,  
RA Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M., Klein C.,  
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
RA Kurita K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,  
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,  
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Takakoshi A., Tanaka T., Terpetra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler B., Wedler H., Weitzenecker T.,  
RA Winters P., Wipac K., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumsstein E., Yoshikawa H., Danchin A.,  
RA "The complete genome sequence of the Gram-positive bacterium Bacillus  
RL subtilis";  
RT Nature 390:249-256(1997).  
RN [3]  
RP CHARACTERIZATION.  
RX MEDLINE=98233759; PubMed=9573215;  
RA Schoenert S., Buder T., Dahl M.K.;  
RT "Identification and enzymatic characterization of the maltose-  
RT inducible alpha-glucosidase Mall (sucrase-isomaltase-maltase) of  
RT Bacillus subtilis";  
RL J. Bacteriol. 180:2574-2578(1998).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=99246561; PubMed=10229946;  
RA Schoenert S., Buder T., Dahl M.K.;  
RT "Properties of maltose-inducible alpha-glucosidase Mall (sucrase-  
RT isomaltase-maltase) in Bacillus subtilis: evidence for its  
RT contribution to maltodextrin utilization";  
RL Res. Microbiol. 150:167-177(1999).  
CC -!- FUNCTION: Hydrolyzes various disaccharides such as sucrose,  
CC maltose, and isomaltose with different efficiencies. Also  
CC hydrolyzes longer maltodextrins from maltotriose up to  
CC maltohexaose, but not maltotriose, palatinose, isomaltotriose,  
CC or isomaltotetraose.  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,6-alpha-D-glucosidic linkages  
CC in some oligosaccharides produced from starch and glycogen by  
CC alpha-amylase, and in isomaltose.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- MISCELLANEOUS: Optimal activity at 42 degrees Celsius.  
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; Z94043; CAB08041.1; -;  
DR EMBL; Z99121; CAB15461.1; -;  
DR PIR; D70034; D70034.  
DR HSP; P21332; IUK.  
DR Subtilast; BG12421; mall.  
DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
DR InterPro; IPR006047; Alpha\_amy1\_cat.  
DR Pfam; PF00128; alpha-amy1ase; 1.  
DR SMART; SM00642; Amy; 1.  
KW Hydrolase; Glycosidase; Complete proteome.  
FT ACT SITE 199 199 BY SIMILARITY.  
FT ACT SITE 255 255 BY SIMILARITY.  
FT ACT SITE 331 331 BY SIMILARITY.  
SQ SEQUENCE 561 AA; 66081 MW; 2B43E9A4AD65A222 CRC64;  
  
Query Match 49.4%; Score 41; DB 1; Length 561;  
Best Local Similarity 53.8%; Pred. No. 55;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 DYSYLQSDPDSF 13  
|||:|:|:  
Db 484 DYQLQENDPQVF 496  
  
RESULT 10  
SNAI HUMAN STANDARD; PRT; 264 AA.  
ID SNAI HUMAN STANDARD; PRT; 264 AA.  
AC Q95863; Q9UBP7; Q9UHH7;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Zinc finger protein SNAI1 (Snail protein homolog) (Sna protein).  
GN SNAI1 OR SNAH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20008744; PubMed=10543399;  
RA Twigg S.R., Wilkie A.O.M.;  
RT "Characterisation of the human snail (SNAI1) gene and exclusion as a  
RT major disease gene in craniosynostosis";  
RL Hum. Genet. 105:320-326(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20008744; PubMed=10543399;  
RA Twigg S.R., Wilkie A.O.M.;  
RT "Characterisation of the human snail (SNAI1) gene and exclusion as a  
RT major disease gene in craniosynostosis";  
RL Hum. Genet. 105:320-326(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20054352; PubMed=10585766;  
RA Paznekas W.A., Okajima K., Scherzer M., Wood S., Jabs E.W.;  
RT "Genomic organization, expression, and chromosome location of the  
RT human SNAI1 gene (SNAI1) and a related processed pseudogene  
RT (SNAI1P)";  
RL Genomics 62:42-49(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21638749; PubMed=11780052;  
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey A.P., Bridgeman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Leivaesalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A., Whitehead S.B., Whittaker P., Willey D.B., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871 (2001).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [6]  
RP SEQUENCE OF 1-172 FROM N.A.  
RX MEDLINE=20122673; PubMed=10655587;  
RA Batlle E., Sancho E., Franci C., Dominguez D., Monfar M., Baulida J., Garcia de Herreiros A.;  
RT "The transcription factor Snail is a repressor of E-cadherin gene expression in epithelial tumour cells.";  
RL Nat. Cell Biol. 2:84-89 (2000).  
CC -!- FUNCTION: SEEMS TO BE INVOLVED IN EMBRYONIC MESODERM FORMATION.  
CC BINDS TO 3 E-BOXES OF THE E-CADHERIN GENE PROMOTER AND REPRESSES ITS TRANSCRIPTION.  
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES WITH THE HIGHEST EXPRESSION IN KIDNEY.  
CC -!- SIMILARITY: BELONGS TO THE SNAIL FAMILY OF ZINC FINGER PROTEINS.  
CC -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF125377; AAD17332.1; -;  
DR EMBL; AJ245657; CAB52414.1; -;  
DR EMBL; AJ245658; CAB52414.1; JOINED.  
DR EMBL; AJ245659; CAB52414.1; JOINED.  
DR EMBL; AF152233; AAD52986.1; -;  
DR EMBL; AF177731; AAD52986.1; -;  
DR EMBL; AL121712; CAC07340.1; -;  
DR EMBL; BC012910; AAI12910.1; -;

DR EMBL; AF131208; AAF32527.1; -;  
DR Genew; HGNC:11128; SNAI1.  
DR MIM; 604238; -;  
DR InterPro; IPR007087; Znf\_C2H2.  
DR Pfam; PF00096; zf-C2H2; 4.  
DR ProDom; PD000003; Znf\_C2H2; 1.  
DR SMART; SM00355; Znf\_C2H2; 4.  
DR PROSITE; PS00028; ZINC FINGER C2H2 1; 3.  
DR PROSITE; PS0157; ZINC FINGER C2H2 2; 4.  
KW Developmental protein; Zinc-finger; Metal-binding; DNA-binding;  
KW Nuclear protein; Repeat.  
FT ZN FING 154 176 C2H2-TYPE 1.  
FT ZN FING 178 202 C2H2-TYPE 2.  
FT ZN FING 208 230 C2H2-TYPE 3.  
FT ZN FING 236 259 C2H2-TYPE 4 (ATYPICAL).  
FT CONFLICT 118 118 V -> A (IN REF. 1).  
FT CONFLICT 154 154 F -> S (IN REF. 6).  
SQ SEQUENCE 264 AA; 29083 MW; 70E298C9BB154115 CRC64;  
Query Match 48.8%; Score 40.5; DB 1; Length 264;  
Best Local Similarity 60.0%; Pred. No. 28;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;  
QY 1 DYSYLOSDPD-SFQ 14  
DB 18 NYSELOSDNPEFTFQ 32  
RESULT 11  
VG03\_BPT4 STANDARD; PRT; 176 AA.  
ID VG03\_BPT4 STANDARD; PRT; 176 AA.  
AC P13331;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tail sheath stabilizing protein Gp3.  
GN 3.  
OS Bacteriophage T4.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
OC T4-like viruses.  
OX NCBI\_TaxID=10665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89123061; PubMed=2644202;  
RA Lipinska B., Rao A.S.M.K., Bolten B.M., Balakrishnan R., Goldberg E.B.;  
RT "Cloning and identification of bacteriophage T4 gene 2 product gp2 and action of gp2 on infecting DNA in vivo.";  
RL J. Bacteriol. 171:488-497 (1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89296504; PubMed=2740234;  
RA Koch T., Lamm N., Rueger W.;  
RT "Sequencing, cloning and overexpression of genes of bacteriophage T4 between map positions 74.325 and 77.184.";  
RL Nucleic Acids Res. 17:4392-4392 (1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22514363; PubMed=12626685;  
RA Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;  
RT "Bacteriophage T4 genome.";  
RL Microbiol. Mol. Biol. Rev. 67:96-156 (2003).  
RN [4]  
RP SEQUENCE OF 57-143 FROM N.A.  
RX MEDLINE=86037230; PubMed=4057254;  
RA Broida J., Abelson J.;  
RT "Sequence organization and control of transcription in the bacteriophage T4 tRNA region.";  
RL J. Mol. Biol. 185:545-563 (1985).  
CC -!- FUNCTION: Involved in phage morphogenesis.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; M23012; AAA50419.1; -;  
DR EMBL; J02516; AAA32496.1; -;  
DR EMBL; AF158101; AAD42439.1; -;  
DR EMBL; X03016; CAA26799.1; -;  
DR EMBL; X14845; CAA32952.1; -;  
DR PIR; C32254; ZREPT9.  
FT CONFLICT 57 63 GRAQRPQ -> ASTTPVV (IN REF. 4).  
FT CONFLICT 71 71 L -> O (IN REF. 4).  
FT CONFLICT 142 143 EF -> RI (IN REF. 4).  
FT CONFLICT 176 176 V -> VLMQPCVL (IN REF. 1).  
SQ SEQUENCE 176 AA; 19712 MW; 34A0887D9D7D9F7F CRC64;

Query Match 48.2%; Score 40; DB 1; Length 176;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DYSYLQSDP 10  
Db :|||:||||  
142 EFSYTEDSDP 151

RESULT 12  
ID SUOE\_BOVIN STANDARD; PRT; 295 AA.  
AC P19217;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Estrogen sulfotransferase (EC 2.8.2.4) (Sulfotransferase, estrogen-  
DE preferring) (STIE1).  
GN STE OR SULTIE1 OR OST.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=90147277; PubMed=3271383;  
RA Nash A.R., Glenn W.K., Moore S.S., Kerr J., Thompson A.R.,  
RA Thompson E.O.P.;  
RT "Oestrogen sulfotransferase: molecular cloning and sequencing of cDNA  
RT for the bovine placental enzyme."  
RL Aust. J. Biol. Sci. 41:507-516(1988).  
RN [2]

RP PARTIAL SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=90104087; PubMed=3270501;  
RA Moore S.S., Thompson E.O.P., Nash A.R.;  
RT "Oestrogen sulfotransferase: isolation of a high specific activity  
RT species from bovine placenta."  
RL Aust. J. Biol. Sci. 41:333-341(1988).  
RN [3]

RP SEQUENCE OF 146-160 AND 206-220, AND CHARACTERIZATION.  
RC TISSUE=Placenta;  
RX MEDLINE=91152101; PubMed=1900200;  
RA Adams J.B.;  
RT "Enzymic synthesis of steroid sulphates. XVII. On the structure of  
RT bovine estrogen sulphotransferase."  
RL Biochim. Biophys. Acta 1076:282-288(1991).  
CC -1- FUNCTION: May control the level of the estrogen receptor by  
CC sulfurylating free estradiol.  
CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + estrone =  
CC adenosine 3',5'-bisphosphate + estrone 3-sulfate.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- INDUCTION: By progesterone.  
CC -1- SIMILARITY: Belongs to the sulfotransferase family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; M54942; AAA30679.1; -;  
DR EMBL; X56395; CAA39806.1; -;  
DR PIR; S29045; S29045.  
DR HSSP; P49891; LAQU.  
DR InterPro; IPR000863; Sulfotransferase.  
DR Pfam; PF00685; Sulfotransferase; 1.  
DR ProDom; PD001218; Sulfotransferase; 1.  
KW Transferase; Phosphorylation; Steroid-binding.  
FT MOD\_RES 216 216 PHOSPHORYLATION (BY PKA) (POTENTIAL).  
FT MOD\_RES 228 228 PHOSPHORYLATION (BY PKA) (POTENTIAL).  
FT CONFLICT 117 117 S -> E (IN REF. 2).  
FT CONFLICT 171 171 S -> E (IN REF. 2).  
FT CONFLICT 248 248 M -> Q (IN REF. 2).  
SQ SEQUENCE 295 AA; 34640 MW; 69147C73146913FD CRC64;

Query Match 48.2%; Score 40; DB 1; Length 295;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DPDSFQD 15  
Db :|||:||||  
151 DPDSFQD 157

RESULT 13  
ID MYCO\_STRCI STANDARD; PRT; 550 AA.  
AC P20910;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Mycolysin precursor (EC 3.4.24.31) (Neutral metalloproteinase) (NPR  
DE (Pronase)).  
GN NPR.  
OS Streptomyces cacaoi.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1898;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=YM15;  
RX MEDLINE=90255973; PubMed=2341042;  
RA Chang P.-C., Kuo T.-C., Tsugita A., Lee Y.-H.W.;  
RT "Extracellular metalloprotease gene of Streptomyces cacaoi:  
RT structure, nucleotide sequence and characterization of the cloned  
RT gene product."  
RL Gene 88:87-95(1990).  
RN [2]  
RP PROCESSING, ACTIVE SITE, ZINC-LIGANDS, AND MUTAGENESIS.  
RX MEDLINE=92156138; PubMed=1740443;  
RA Chang P.-C., Lee Y.-H.W.;  
RT "Extracellular autoprocesing of a metalloprotease from Streptomyces  
RT cacaoi."  
RL J. Biol. Chem. 267:3952-3958(1992).  
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of bonds with  
CC hydrophobic residues in P1'.  
CC -1- COFACTOR: Binds 1 zinc ion.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to peptidase family M5.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; M37055; AAA26789.1; -  
DR PIR; JQ0530; HYSMCA.  
DR MEROPS; M05.001; -  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR000437; Prok\_lipoprot\_S.  
DR PROSITE; PS00142; ZINC PROTEASE; FALSE NEG.  
KW Hydrolase; Metalloprotease; Zinc; Zymogen; Signal.  
FT SIGNAL 1 34  
FT PROPEP 35 205 MYCOLYSIN  
FT CHAIN 206 550 ZINC (CATALYTIC).  
FT METAL 407 407  
FT ACT\_SITE 408 408  
FT METAL 411 411 ZINC (CATALYTIC).  
FT METAL 445 445 ZINC (CATALYTIC).  
SQ SEQUENCE 550 AA; 58678 MW; C9FF9C998044D8BE CRC64;

Query Match 48.2%; Score 40; DB 1; Length 550;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DYSYLQSDSDPS 12  
Db 390 DKVHLADSDPS 401

RESULT 14  
ID\_VG28 BPML5 STANDARD; PRT; 595 AA.  
AC Q05235;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE Minor tail protein GP28.  
GN 28.  
OS Mycobacteriophage L5.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC L5-like viruses.  
OX NCBI\_TaxID=31757;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.  
RX MEDLINE=93211282; PubMed=8459766;  
RA Hatfull G.F., Sarkis G.J.;  
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
RL a phage system for mycobacterial genetics.";  
RL Mol. Microbiol. 7:395-405(1993).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; Z18946; CAA79404.1; -  
DR PIR; S30973; S30973.  
DR INIT MET 0  
SQ SEQUENCE 595 AA; 66789 MW; 679132A2644B9142 CRC64;  
Query Match 48.2%; Score 40; DB 1; Length 595;  
Best Local Similarity 50.0%; Pred. No. 84;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YLQSDSDPSFOD 15  
Db 245 YIKORDPHFPED 256

RESULT 15  
ASM\_HUMAN STANDARD; PRT; 629 AA.  
ID\_P17405; P17406; Q13811; Q16837; Q16841;  
AC DT 01-AUG-1990 (Rel. 15, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Sphingomyelin phosphodiesterase precursor (EC 3.1.4.12) (Acid  
DE sphingomyelinase) (asMase).  
GN SMPD1 OR ASM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=91217097; PubMed=1840600;  
RA Schuchman E.H., Suchi M., Takahashi T., Sandhoff K., Desnick R.J.;  
RT "Human acid sphingomyelinase. Isolation, nucleotide sequence and  
RT expression of the full-length and alternatively spliced cDNAs.";  
RL J. Biol. Chem. 266:8531-8539(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93183402; PubMed=1292508;  
RA Newrzella D., Stoffel W.;  
RT "Molecular cloning of the acid sphingomyelinase of the mouse and the  
RT organization and complete nucleotide sequence of the gene.";  
RL Biol. Chem. Hoppe-Seyler 373:1233-1238(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92155708; PubMed=1740330;  
RA Schuchman E.H., Levran O., Pereira L.V., Desnick R.J.;  
RT "Structural organization and complete nucleotide sequence of the gene  
RT encoding human acid sphingomyelinase (SMPD1).";  
RL Genomics 12:197-205(1992).  
RN [4]  
RP SEQUENCE FROM N.A., AND VARIANT ARG-157.  
RX MEDLINE=94012573; PubMed=8407868;  
RA Ida H., Rennert O.M., Eto Y., Chan W.Y.;  
RT "Cloning of a human acid sphingomyelinase cDNA with a new mutation  
RT that renders the enzyme inactive.";  
RL J. Biochem. 114:15-20(1993).  
RN [5]  
RP SEQUENCE OF 128-629 FROM N.A., PARTIAL SEQUENCE, AND  
RP ALTERNATIVE SPLICING.  
RC TISSUE=Fibroblast;  
RX MEDLINE=90060003; PubMed=2555181;  
RA Quintern L.E., Schuchman E.H., Levran O., Suchi M., Ferlinz K.,  
RA Reinke H., Sandhoff K., Desnick R.J.;  
RT "Isolation of cDNA clones encoding human acid sphingomyelinase:  
RT occurrence of alternatively processed transcripts.";  
RL EMBO J. 8:2469-2473(1989).  
RN [6]  
RP CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=97182640; PubMed=9030779;  
RA Ferlinz K., Hurwitz R., Moczall H., Lansmann S., Schuchman E.H.,  
RA Sandhoff K.;  
RT "Functional characterization of the N-glycosylation sites of human  
RT acid sphingomyelinase by site-directed mutagenesis.";  
RL Eur. J. Biochem. 243:511-517(1997).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE=22518502; PubMed=12631268;  
RA Lansmann S., Schuette C.G., Bartelsen O., Hoernschemeyer J., Linke T.,  
RA Weisgerber J., Sandhoff K.;  
RT "Human acid sphingomyelinase.";  
RL Eur. J. Biochem. 270:1076-1088(2003).  
RN [8]  
RP VARIANT NPA SER-577.  
RX MEDLINE=92028849; PubMed=1718266;  
RA Ferlinz K., Hurwitz R., Sandhoff K.;  
RT "Molecular basis of acid sphingomyelinase deficiency in a patient



with Niemann-Pick disease type A.";  
RN Biochem. Biophys. Res. Commun. 179:1187-1191(1991).  
[9]  
RP VARIANT NPA LEU-496.  
RX MEDLINE=91219449; PubMed=2023926;  
RA Levran O., Desnick R.J., Schuchman E.H.;  
RT "Niemann-Pick disease: a frequent missense mutation in the acid  
RT sphingomyelinase gene of Ashkenazi Jewish type A and B patients.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:3748-3752(1991).  
[10]  
RP VARIANT NPB ARG-608 DEL.  
RX MEDLINE=91358737; PubMed=1885770;  
RA Levran O., Desnick R.J., Schuchman E.H.;  
RT "Niemann-Pick type B disease. Identification of a single codon  
RT deletion in the acid sphingomyelinase gene and genotype/phenotype  
RT correlations in type A and B patients.";  
RL J. Clin. Invest. 88:806-810(1991).  
[11]  
RP VARIANT NPA PRO-302.  
RX MEDLINE=93004773; PubMed=1391960;  
RA Levran O., Desnick R.J., Schuchman E.H.;  
RT "Identification and expression of a common missense mutation (L302P)  
RT in the acid sphingomyelinase gene of Ashkenazi Jewish type A  
RT Niemann-Pick disease patients.";  
RL Blood 80:2081-2087(1992).  
[12]  
RP VARIANT NPB ARG-436.  
RX MEDLINE=93244834; PubMed=1301192;  
RA Takahashi T., Desnick R.J., Takada G., Schuchman E.H.;  
RT "Identification of a missense mutation (S436R) in the acid  
RT sphingomyelinase gene from a Japanese patient with type B  
RT Niemann-Pick disease.";  
RL Hum. Mutat. 1:70-71(1992).  
[13]  
RP VARIANT NPA ILE-382, AND VARIANTS NPB ARG-242 AND SER-383.  
RX MEDLINE=93216934; PubMed=1618760;  
RA Takahashi T., Suchi M., Desnick R.J., Takada G., Schuchman E.H.;  
RT "Identification and expression of five mutations in the human acid  
RT sphingomyelinase gene causing types A and B Niemann-Pick disease.  
RT Molecular evidence for genetic heterogeneity in the neuronopathic and  
RT non-neuronopathic forms.";  
RL J. Biol. Chem. 267:12552-12558(1992).  
[14]  
RP VARIANT NPB GLY-391.  
RX MEDLINE=94328611; PubMed=8051942;  
RA Sperl W., Bart G., Vanier M.T., Christomanou H., Baldissera I.,  
RA Steichensdorf E., Paschke E.;  
RT "A family with visceral course of Niemann-Pick disease, macular halo  
RT syndrome and low sphingomyelin degradation rate.";  
RL J. Inher. Metab. Dis. 17:93-103(1994).  
[15]  
RP VARIANT NPA THR-389.  
RX MEDLINE=96287387; PubMed=8680412;  
RA Schuchman E.H.;  
RT "Two new mutations in the acid sphingomyelinase gene causing type A  
RT Niemann-Pick disease: N389T and R441X.";  
RL Hum. Mutat. 6:352-354(1995).  
[16]  
RP VARIANT NPA CYS-446.  
RX MEDLINE=96274768; PubMed=8693491;  
RA Takahashi T., Suchi M., Sato W., Ten S.B., Sakuragawa N.,  
RA Desnick R.J., Schuchman E.H., Takada G.;  
RT "Identification and expression of a missense mutation (Y446C) in the  
RT acid sphingomyelinase gene from a Japanese patient with type A  
RT Niemann-Pick disease.";  
RL Tohoku J. Exp. Med. 177:117-123(1995).  
[17]  
RP VARIANT NPA GLN-246.  
RX MEDLINE=96263741; PubMed=8664904;  
RA Ida H., Rennert O.M., Maekawa K., Eto Y.;  
RT "Identification of three novel mutations in the acid  
RT sphingomyelinase gene of Japanese patients with Niemann-Pick disease  
RT type A and B."

Hum. Mutat. 7:65-67(1996).  
[18]  
RP VARIANT NPB TYR-421.  
RX MEDLINE=22340429; PubMed=12369017;  
RA Simonaro C.M., Desnick R.J., McGovern M.M., Wasserstein M.P.,  
RA Schuchman E.H.;  
RT "The demographics and distribution of type B Niemann-Pick disease:  
RT novel mutations lead to new genotype/phenotype correlations.";  
RL Am. J. Hum. Genet. 71:1413-1419(2002).  
[19]  
RP VARIANTS NPA ARG-248; TYR-319; SER-463; LEU-475 AND HIS-537, AND  
RP VARIANTS NPB SER-371 AND ARG-608 DEL.  
RX MEDLINE=22444008; PubMed=12556236;  
RA Sikora J., Pavli-Pereira H., Ellender M., Roelofs H., Wevers R.A.;  
RT "Seven novel Acid sphingomyelinase gene mutations in Niemann-Pick type  
RT A and B patients.";  
RL Am. Hum. Genet. 67:63-70(2003).  
CC -!- FUNCTION: Converts sphingomyelin to ceramide. ASM also has  
CC phospholipase C activities toward 1,2-diacylglycerolphosphocholine  
CC and 1,2-diacylglycerolphosphoglycerol.  
CC -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acylsphingosine +  
CC choline phosphate.  
CC -!- SUBUNIT: Monomer.  
CC -!- SUBCELLULAR LOCATION: Lysosomal.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=1; Synonyms=ASM-1;  
CC IsoId=P17405-1; Sequence=Displayed;  
CC Name=2; Synonyms=ASM-2;  
CC IsoId=P17405-2; Sequence=VSP\_000331, VSP\_000332;  
CC Name=3; Synonyms=ASM-3;  
CC IsoId=P17405-3; Sequence=VSP\_000333;  
CC -!- DISEASE: Defects in SMPD1 are the cause of Niemann-Pick disease  
CC type A (NPA) [MIM:257200]; also referred to as the classical  
CC infantile form. Niemann-Pick disease is a clinically and  
CC genetically heterogeneous recessive disorder. It is caused by the  
CC accumulation of sphingomyelin and other metabolically related  
CC lipids in the lysosomes, resulting in neurodegeneration starting  
CC from early life. Patients may show xanthomas, pigmentation,  
CC hepatosplenomegaly, lymphadenopathy and mental retardation.  
CC Niemann-Pick disease occurs more frequently among individuals of  
CC Ashkenazi Jewish ancestry than in the general population. NPA is  
CC characterized by very early onset in infancy and a rapidly  
CC progressive course leading to death by three years.  
CC -!- DISEASE: Defects in SMPD1 are the cause of Niemann-Pick disease  
CC type B (NPB) [MIM:607616]; also referred to as the visceral form.  
CC NPB has little if any neurologic involvement and patients may  
CC survive into adulthood.  
CC -!- MISCELLANEOUS: There are two types of sphingomyelinases: ASM  
CC (acid), and NSM (neutral).  
CC -!- MISCELLANEOUS: Isoform 1 is the most abundant (90%), isoforms 2  
CC (10%) and 3 (<1%) are only found at lower levels. Only isoform 1  
CC is a catalytic active enzyme.  
CC -!- SIMILARITY: Belongs to the acid sphingomyelinase family.  
CC -!- SIMILARITY: Contains 1 saposin B-type domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

Query Match 48.2%; Score 40; DB 1; Length 629;

Best Local Similarity 54.5%; Pred. No. 90;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYSVLQSDSDP 11

Db 210 DHLYEGTDPD 220

Search completed: June 3, 2004, 15:14:46

Job time : 11 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:24 ; Search time 36.5 Seconds  
(without alignments)  
129.665 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DYSYLQSDPDPSFQD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mhc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp.rodent:\*
- 12: sp.virus:\*
- 13: sp.vertebrate:\*
- 14: sp.unclassified:\*
- 15: sp.rvirus:\*
- 16: sp.bacteriap:\*
- 17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	134	4	Q15677
2	83	100.0	134	6	Q9GLU9
3	83	100.0	134	6	Q9GLU5
4	83	100.0	134	6	Q9GLS9
5	83	100.0	135	6	Q9GLU1
6	83	100.0	135	6	Q9GLU3
7	83	100.0	529	6	Q9BDE0
8	78	94.0	134	6	Q9GLT1
9	75	90.4	135	6	Q9GLT3
10	75	90.4	135	6	Q9GLR7
11	75	90.4	135	6	Q9GLS5
12	75	90.4	135	6	Q9GLV1
13	75	90.4	135	6	Q9GLR9
14	75	90.4	135	6	Q9GLS1
15	75	90.4	135	6	Q9GLT5
16	75	90.4	135	6	Q9GLS7

17	75	90.4	135	6	Q9GLS3
18	73	88.0	530	6	Q8WN56
19	73	88.0	530	6	Q8MIU0
20	72	86.7	135	6	Q9GLU7
21	71	85.5	530	6	Q9MYI7
22	68	81.9	135	6	Q9GLV3
23	68	81.9	135	6	Q9GLM9
24	68	81.9	135	6	Q9GLT9
25	68	81.9	135	6	Q9GLT7
26	68	81.9	135	6	Q9GLM5
27	68	81.9	135	6	Q9GLM7
28	54	65.1	533	11	Q91XK0
29	51	61.4	530	6	Q7YR88
30	49	59.0	308	11	Q8CIT7
31	49	59.0	336	17	Q28939
32	49	59.0	353	4	Q8IY68
33	48	57.8	696	4	Q96SP9
34	48	57.8	696	11	Q810C1
35	46	55.4	760	4	Q96PX8
36	46	55.4	340	4	Q8N8I8
37	45	54.2	232	16	Q8XHI5
38	45	54.2	309	16	Q8CUQ2
39	45	54.2	393	16	Q92BB8
40	45	54.2	393	16	Q8YJ00
41	45	54.2	476	10	Q9SIB2
42	45	54.2	476	10	Q8LFQ0
43	45	54.2	527	13	Q9PSV0
44	45	54.2	529	13	Q91436
45	45	54.2	529	13	Q8UUC5

#### ALIGNMENTS

#### RESULT 1

Q15677 Q15677 PRELIMINARY; PRT; 134 AA.  
 AC Q15677; (Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last annotation update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Tyrosinase-related gene segment, exon 5 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91236163; PubMed=1903356;  
 RA Giebel L.B., Strunk K.M., Spritz R.A.;  
 RT "Organization and nucleotide sequences of the human tyrosinase gene  
 and a truncated tyrosine-related segment";  
 RL Genomics 9:435-445(1991).  
 DR EMBL; M63241; AAA73001.1; JOINED.  
 DR EMBL; M63240; AAA73001.1; JOINED.  
 DR Genew; HGNC:12443; TYRL.  
 DR GO; GO:0016491; P:oxidoreductase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR008922; Di-copper centre.  
 DR InterPro; IPR002227; Tyrosinase.  
 DR Pfam; PF00264; tyrosinase; 1.  
 DR NON\_TER 1  
 SQ SEQUENCE 134 AA; 15770 MW; 7438E1B960DB9A CRC64;

Query Match 100.0%; Score 83; DB 4; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 15; Conservative 0;

QY 1 DYSYLQSDPDPSFQD 15

Db 53 DYSYLQSDPDPSFQD 67

```
RESULT 2
Q9GLU9 PRELIMINARY; PRT; 134 AA.
ID Q9GLU9
AC Q9GLU9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183591; AAG26323.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 134 AA; 15754 MW; 7428A1BAF97CDB9A CRC64;

Query Match 100.0%; Score 83; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15
Db |||||
53 DYSYLQSDPDPSFQD 67

RESULT 3
Q9GLU5 PRELIMINARY; PRT; 134 AA.
ID Q9GLU5
AC Q9GLU5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183603; AAG27272.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 134 AA; 15754 MW; 7428A1BAF97CDB9A CRC64;

Query Match 100.0%; Score 83; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15
Db |||||
53 DYSYLQSDPDPSFQD 67

RESULT 4
Q9GLS9 PRELIMINARY; PRT; 134 AA.
ID Q9GLS9
AC Q9GLS9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9597;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183653; AAG27279.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 134 AA; 15754 MW; 7428A1BAF97CDB9A CRC64;

Query Match 100.0%; Score 83; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15
Db |||||
53 DYSYLQSDPDPSFQD 67

RESULT 5
Q9GLU1 PRELIMINARY; PRT; 135 AA.
ID Q9GLU1
AC Q9GLU1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Hylobates leucogenys (White-cheeked gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=61853;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183613; AAG28345.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 135 AA; 15839 MW; AAD2FCE175EF37DB CRC64;

Query Match 100.0%; Score 83; DB 6; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15
Db |||||
53 DYSYLQSDPDPSFQD 67
```

```
QY 1 DYSYLQSDPDSFQD 15
Db 53 DYSYLQSDPDSFQD 67

RESULT 6
Q9GLU3 PRELIMINARY; PRT; 135 AA.
AC Q9GLU3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Hylobates hoolek (Hoolock gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=61851;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183608; AAG28343.1; -.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR Pfam; PF00264; tyrosinase; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 135 AA; 15867 MW; AAD2FCE02BF5866B CRC64;

Query Match 100.0%; Score 83; DB 6; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSFQD 15
Db 53 DYSYLQSDPDSFQD 67

RESULT 7
Q9BDE0 PRELIMINARY; PRT; 529 AA.
AC Q9BDE0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Snowflake, Ndengue, and Machinda;
RA Martinez-Arias R., Comas D., Bertranpetit J.;
RT "Tyrosinase gene in gorilla and the albinism of Snowflake.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237806; AAK00804.1; -.
DR EMBL; AF237802; AAK00804.1; JOINED.
DR EMBL; AF237803; AAK00804.1; JOINED.
DR EMBL; AF237804; AAK00804.1; JOINED.
DR EMBL; AF237805; AAK00804.1; JOINED.
DR EMBL; AF237796; AAK00802.1; -.
DR EMBL; AF237792; AAK00802.1; JOINED.
DR EMBL; AF237793; AAK00802.1; JOINED.
DR EMBL; AF237794; AAK00802.1; JOINED.
DR EMBL; AF237795; AAK00802.1; JOINED.
DR EMBL; AF237801; AAK00803.1; -.

Query Match 100.0%; Score 83; DB 6; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSFQD 15
Db 53 DYSYLQSDPDSFQD 67

RESULT 8
Q9GLT1 PRELIMINARY; PRT; 134 AA.
AC Q9GLT1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183648; AAG27278.1; -.
DR EMBL; AF183647; AAG27278.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR Pfam; PF00264; tyrosinase; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 134 AA; 15823 MW; 1E8D060520CDB9B CRC64;

Query Match 100.0%; Score 83; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSFQD 15
Db 448 DYSYLQSDPDSFQD 462

RESULT 9
Q9GLT3 PRELIMINARY; PRT; 135 AA.
AC Q9GLT3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```

```
DR EMBL; AF237797; AAK00803.1; JOINED.
DR EMBL; AF237798; AAK00803.1; JOINED.
DR EMBL; AF237799; AAK00803.1; JOINED.
DR EMBL; AF237800; AAK00803.1; JOINED.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
DR PRINTS; PR00092; TYROSINASE.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
DR PROSITE; PS00497; TYROSINASE_1; 1.
DR PROSITE; PS00498; TYROSINASE_2; 1.
SQ SEQUENCE 529 AA; 60418 MW; 49FEF77DADE161A2 CRC64;

Query Match 100.0%; Score 83; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSFQD 15
Db 448 DYSYLQSDPDSFQD 462

RESULT 8
Q9GLT1 PRELIMINARY; PRT; 134 AA.
AC Q9GLT1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183648; AAG27278.1; -.
DR EMBL; AF183647; AAG27278.1; JOINED.
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008922; Di-copper_centre.
DR InterPro; IPR002227; Tyrosinase.
DR Pfam; PF00264; tyrosinase; 1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 134 AA; 15823 MW; 1E8D060520CDB9B CRC64;

Query Match 94.0%; Score 78; DB 6; Length 134;
Best Local Similarity 93.3%; Pred. No. 2.2e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSFQD 15
Db 53 DYSYLQSDPDSFQD 67

RESULT 9
Q9GLT3 PRELIMINARY; PRT; 135 AA.
AC Q9GLT3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```

DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OS Nasalis larvatus (Proboscis monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Nasalis.  
 OX NCBI\_TaxID=43780;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183643; AAC27275.1;  
 DR EMBL; AF183642; AAC27275.1; JOINED.  
 DR GO: GO:0004503; F:monophenol monooxygenase activity; IEA.  
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO: GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR008922; Di-copper\_centre.  
 DR Pfam; PF00264; Tyrosinase.  
 DR Oxidoreductase.  
 KW Oxidoreductase.  
 FT NON\_TER 1  
 SQ SEQUENCE 135 AA; 15690 MW; FE9070222D41FA88 CRC64;  
 Query Match 90.4%; Score 75; DB 6; Length 135;  
 Best Local Similarity 93.3%; Pred. No. 7.3e-05;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDSDSFQD 15  
 DB 53 DYSYLQSDSDSFQD 67  
 RESULT 10  
 Q9GLR7 PRELIMINARY; PRT; 135 AA.  
 AC Q9GLR7  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Pygathrix.  
 OX NCBI\_TaxID=61621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183688; AAC33683.1;  
 DR EMBL; AF183687; AAC33683.1; JOINED.  
 DR GO: GO:0004503; F:monophenol monooxygenase activity; IEA.  
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO: GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR008922; Di-copper\_centre.  
 DR InterPro; IPR002227; Tyrosinase.  
 DR Pfam; PF00264; tyrosinase; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 1  
 SQ SEQUENCE 135 AA; 15686 MW; FE90643B963855E8 CRC64;  
 Query Match 90.4%; Score 75; DB 6; Length 135;  
 Best Local Similarity 93.3%; Pred. No. 7.3e-05;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYLQSDSDSFQD 15  
 DB 53 DYSYLQSDSDSFQD 67

RESULT 11  
 Q9GLS5

ID Q9GLS5 PRELIMINARY; PRT; 135 AA.  
 AC Q9GLS5  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OS Trachypithecus phayrei (Phayre's leaf monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Trachypithecus.  
 OX NCBI\_TaxID=61618;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183668; AAC29588.1;  
 DR EMBL; AF183667; AAC29588.1; JOINED.  
 DR GO: GO:0004503; F:monophenol monooxygenase activity; IEA.  
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO: GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR008922; Di-copper\_centre.  
 DR InterPro; IPR002227; Tyrosinase.  
 DR Pfam; PF00264; tyrosinase; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 1  
 SQ SEQUENCE 135 AA; 15656 MW; FE90702F962C41E8 CRC64;  
 Query Match 90.4%; Score 75; DB 6; Length 135;  
 Best Local Similarity 93.3%; Pred. No. 7.3e-05;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYLQSDSDSFQD 15  
 DB 53 DYSYLQSDSDSFQD 67

RESULT 12

Q9GLV1 PRELIMINARY; PRT; 135 AA.  
 AC Q9GLV1  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OS Papio hamadryas (Hamadryas baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Papio.  
 OX NCBI\_TaxID=9557;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183587; AAC21893.1;  
 DR EMBL; AF183586; AAC21893.1; JOINED.  
 DR GO: GO:0004503; F:monophenol monooxygenase activity; IEA.  
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO: GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR008922; Di-copper\_centre.  
 DR InterPro; IPR002227; Tyrosinase.  
 DR Pfam; PF00264; tyrosinase; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 1  
 SQ SEQUENCE 135 AA; 15685 MW; EBD1303B963855E8 CRC64;

Query Match 90.4%; Score 75; DB 6; Length 135;  
 Best Local Similarity 93.3%; Pred. No. 7.3e-05;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYLQSDSDSFQD 15  
 DB 53 DYSYLQSDSDSFQD 67

Ds 53 DYSYLQSDSDSFQD 67

## RESULT 13

Q9GLR9 Q9GLR9 PRELIMINARY; PRT; 135 AA.  
AC Q9GLR9;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Tyrosinase (EC 1.14.18.1) (Fragment).  
OS Trachypithecus leucocephalus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
OC Trachypithecus.  
OX NCBI\_TaxID=61617;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
RT "Molecular evolution of tyrosinase gene in primates."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF183683; AAG33681.1; -  
DR EMBL; AF183682; AAG33681.1; JOINED.  
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR008922; Di-copper centre.  
DR InterPro; IPR002227; Tyrosinase.  
DR Pfam; PF00264; tyrosinase; 1.  
KW Oxidoreductase.  
FT NON\_TER 1  
SQ SEQUENCE 135 AA; 15656 MW; FE90702F962C41E8 CRC64;

Query Match 90.4%; Score 75; DB 6; Length 135;  
Best Local Similarity 93.3%; Pred. No. 7.3e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYLQSDSDSFQD 15

Db 53 DYSYLQSDSDSFQD 67

## RESULT 14

Q9GLS1 Q9GLS1 PRELIMINARY; PRT; 135 AA.  
AC Q9GLS1;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Tyrosinase (EC 1.14.18.1) (Fragment).  
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
OC Trachypithecus.  
OX NCBI\_TaxID=54180;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
RT "Molecular evolution of tyrosinase gene in primates."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF183678; AAG33679.1; -  
DR EMBL; AF183677; AAG33679.1; JOINED.  
DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR008922; Di-copper centre.  
DR InterPro; IPR002227; Tyrosinase.  
DR Pfam; PF00264; tyrosinase; 1.  
KW Oxidoreductase.  
FT NON\_TER 1  
SQ SEQUENCE 135 AA; 15656 MW; FE90702F962C41E8 CRC64;

Query Match 90.4%; Score 75; DB 6; Length 135;

Best Local Similarity 93.3%; Pred. No. 7.3e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYLQSDSDSFQD 15

Db 53 DYSYLQSDSDSFQD 67

## RESULT 15

Q9GLT5 Q9GLT5 PRELIMINARY; PRT; 135 AA.  
AC Q9GLT5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Tyrosinase (Fragment).  
OS Pysathrix avunculus (Tonkin snub-nosed monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
OC Pysathrix.  
OX NCBI\_TaxID=66062;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
RT "Molecular evolution of tyrosinase gene in primates."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF183638; AAG27273.1; -  
DR EMBL; AF183637; AAG27273.1; JOINED.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR008922; Di-copper centre.  
DR InterPro; IPR002227; Tyrosinase.  
DR Pfam; PF00264; tyrosinase; 1.  
FT NON\_TER 1  
SQ SEQUENCE 135 AA; 15656 MW; FE90702F962C41E8 CRC64;

Query Match 90.4%; Score 75; DB 6; Length 135;  
Best Local Similarity 93.3%; Pred. No. 7.3e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYLQSDSDSFQD 15

Db 53 DYSYLQSDSDSFQD 67

Search completed: June 3, 2004, 15:14:11  
Job time : 36.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 17:08:58 ; Search time 55 Seconds  
(without alignments)  
77.058 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462  
Perfect score: 83  
Sequence: 1 DYSYLQSDPDPSFQD 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	15	2	AAW15323 Class II
2	83	100.0	15	2	AAW33169 Human tyr
3	83	100.0	15	2	AAW00711 Tumour an
4	83	100.0	15	2	AAW49659 Tumour an
5	83	100.0	15	2	AAW01749 Exemplary
6	83	100.0	15	3	AAW1516 Human Tyr
7	83	100.0	15	3	AAW90800 Human leu
8	83	100.0	15	3	AAW23672 Cytotoxic
9	83	100.0	15	3	AAW92296 Tyrosinas
10	83	100.0	15	3	AAW56611 Tyrosinas
11	83	100.0	15	3	AAW84292 Tumour as
12	83	100.0	15	3	AAW82975 Tyrosinas
13	83	100.0	15	3	AAW02618 Tumour as
14	83	100.0	15	3	AAW08690 Antigenic
15	83	100.0	15	4	AAW02107 Tyrosinas
16	83	100.0	15	4	AAW31350 Exemplary
17	83	100.0	15	5	AAW06837 Human tyr
18	83	100.0	15	5	AAW9140 Human tyr
19	83	100.0	15	6	AAW19544 Human can
20	83	100.0	30	5	AAW84918 Human can
21	83	100.0	508	2	AAW38167 Mutant hu
22	83	100.0	529	2	AAW56309 Human tyr
23	83	100.0	529	2	AAW63623 Human tyr
24	83	100.0	529	2	AAW00184 Human tyr
25	83	100.0	529	2	AAW03306 Tyrosinas

26	83	100.0	529	2	AAW38166 Normal hu
27	83	100.0	529	2	AAW36519 Tyrosinas
28	83	100.0	529	2	AAW71234 Tyrosinas
29	83	100.0	529	4	AAW51344 Human tyr
30	83	100.0	529	4	AAW86039 Human tyr
31	83	100.0	529	5	AAW84806 Human tyr
32	83	100.0	529	5	AAW11544 Human mel
33	83	100.0	529	6	ABP74129 Human tyr
34	83	100.0	529	6	ABR83439 Human tyr
35	83	100.0	529	7	ADC09566 Tyrosinas
36	83	100.0	531	2	AAW07071 Sequence
37	83	100.0	531	2	AAW79493 Human tyr
38	83	100.0	531	2	AAW22083 Human SK2
39	83	100.0	560	2	AAW38165 Human tyr
40	83	100.0	5546	5	AAW85008 Human mel
41	79	95.2	15	2	AAW15354 Class II
42	79	95.2	15	2	AAW15331 Class II
43	79	95.2	15	2	AAW15332 Class II
44	77	92.8	14	2	AAW15324 Class II
45	77	92.8	15	2	AAW15353 Class II

## ALIGNMENTS

RESULT 1  
AAW15323  
ID AAW15323 standard; peptide; 15 AA.  
XX  
AC AAW15323;  
XX  
DT 09-FEB-1998 (first entry)  
XX  
DE Class II restricted melanoma tyrosinase derived antigenic peptide 3.  
XX  
KW Major histocompatibility complex; MHC; Class II; tyrosinase; vaccine;  
KW immune response; immunogenic peptide; melanoma; treatment;  
KW protective antibody; immune cells; CD8+ T cell; CD4+ T cell.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9711669-A2.  
XX  
PD 03-APR-1997.  
XX  
PF 25-SEP-1996; 96WO-US015346.  
XX  
PR 26-SEP-1995; 95US-00533895.  
XX  
(USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Topalian SL, Rosenberg SA, Robbins PF;  
XX  
DR WPI; 1997-212652/19.  
XX  
PT Major histocompatibility complex Class H immunogenic peptide - used to prevent or treat melanoma in mammal by stimulating production of protective antibodies or immune cells.  
XX  
PS Claim 2; Page 59; 79pp; English.  
XX  
CC Peptides AAW15321-56 are major histocompatibility complex (MHC) Class II restricted melanoma peptides, derived from tyrosinase. Tumour reactive human CD4+ and CD8+ T cells recognise melanoma antigens encoded by the tyrosinase gene. The present sequence is derived from amino acids 448-462. The peptides may be used as a vaccine, either prophylactically in advance of any evidence of melanoma, or therapeutically to enhance the patients own immune response. The immunogenic peptides can be used to prevent or treat melanoma in a mammal by stimulating the production of protective antibodies or immune cells, preferably immune positive CD4+ T cells

SQ Sequence 15 AA;  
Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15  
| | | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPDQ 15

RESULT 2  
AAY33169  
ID AAY33169 standard; peptide; 15 AA.  
XX AC AAY33169;  
XX AC AAY33169;  
XX AC AAY33169;  
DT 17-NOV-1999 (first entry)  
XX DE Human tyrosinase peptide #8.  
XX KW Human; protein delivery; Yersinia sp; effector gene; mutant; antigen;  
XX KW immune response; cytotoxic T-lymphocyte; CTL; vaccination; treatment;  
XX KW pathological disorder; tyrosinase.  
XX OS Homo sapiens.  
XX PN WO9945098-A2.  
XX PD 10-SEP-1999.  
XX PF 03-MAR-1999; 99WO-IB000587.  
XX PR 06-MAR-1998; 98US-00036582.  
XX PA (VBRU/) VAN DER BRUGGEN P B.  
XX PA (CORN/) CORNELIS G R.  
XX PA (BOLA/) BOLAND A M.  
XX PA (BOON/) BOON-FALLEUR T R.  
XX PI Van Der Bruggen PB, Cornelis GR, Boland AM, Boon-Falleur TR;  
XX WPI; 1999-540840/45.  
XX DR New mutant Yersinia strains useful for treating a pathological disorder.  
XX PT Example 1 ; Page 70; 80pp; English.  
XX PS This invention describes a novel mutant Yersinia (Y1) strain, comprising  
XX CC mutation(s) in effector-encoding gene(s) and deficient in the production  
XX CC of functional effector protein(s). The invention describes (1) a  
XX CC quintuple mutant Yersinia strain, having the designation Yersinia  
XX CC enterocolitica yopBOMP or Yersinia pseudotuberculosis yopBHAOJ; (2) an  
XX CC expression vector (EV1) for delivering a heterologous protein into a  
XX CC eukaryotic cell, comprising in the 5'-3' direction; (3) a Yersinia or  
XX CC mutant Yersinia strain for delivering a heterologous protein into a  
XX CC eukaryotic cell, comprising contacting the cell with a Y1 transformed  
XX CC with the above vector (Y1-EV1); (4) a method for delivering a  
XX CC heterologous protein into a eukaryotic cell, comprising contacting the  
XX CC cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method  
XX CC for inducing an immune response specific for a heterologous protein; (6)  
XX CC a method for inducing a cytotoxic T-lymphocyte (CTL) response specific  
XX CC for a heterologous protein; (7) a method for determining the efficacy of  
XX CC an antigen vaccination regimen in a subject. Y1 is used to treat a  
XX CC pathological disorder, by providing recombinant Yersinia for the safe  
XX CC delivery of proteins into eukaryotic cells. AAY33147-Y33178 are human-  
XX CC derived peptides used to illustrate the method of the invention

SQ Sequence 15 AA;  
Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15  
| | | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPDQ 15

RESULT 3  
AAY00711  
ID AAY00711 standard; peptide; 15 AA.  
XX AC AAY00711;  
XX AC AAY00711;  
DT 12-MAY-1999 (first entry)  
XX DE Tumour antigen booster peptide Tyrosinase HLA-DR4.  
XX KW Tumour antigen; booster peptide; immune response modulation; allergy;  
XX KW immune response enhancer; tumour cell; tumour rejection antigen;  
XX KW leukocyte antigen-presenting molecule; autoimmune disease;  
XX KW allograft rejection.  
XX OS Homo sapiens.  
XX PN WO9858956-A2.  
XX PD 30-DEC-1998.  
XX PF 19-JUN-1998; 98WO-US012894.  
XX PR 23-JUN-1997; 97US-00880979.  
XX PA (LUDW-) LUDWIG INST CANCER RES.  
XX PI Warnier G, Uyttenhove C, Boon-Falleur T;  
XX WPI; 1999-105612/09.  
XX DR Immunization methods using viruses expressing antigen for priming and  
XX PT booster immunizations - useful for modulating immune responses against  
XX PT antigen, e.g. enhancing immune response against tumour cells expressing  
XX PT tumour rejection antigens.  
XX PS Disclosure; Page 9; 33pp; English.  
XX CC This sequence represents a tumour antigen booster peptide that can be  
XX CC used in the method of the invention. The method is for modulating an  
XX CC immune response in a mammal against an antigen, and comprises: (A)  
XX CC inducing an immune response by: (i) administering a virus containing a  
XX CC nucleic acid molecule encoding the antigen or its precursor to generate  
XX CC an immune response; and (ii) administering at least one booster dose  
XX CC comprising a peptide including the antigen, in an adjuvant, in a combined  
XX CC amount effective to enhance the initial immune response; or (B) reducing  
XX CC an immune response as defined for (A) but using a non-adjuvant with the  
XX CC peptide which includes the antigen, in an amount effective to reduce the  
XX CC initial immune response. Method (A) is used to enhance the immune  
XX CC response against tumour cells expressing tumour rejection antigens, and  
XX CC against pathogens in subjects having human leukocyte antigen-presenting  
XX CC molecules. Method (B) is used to reduce the immune response in allergy,  
XX CC autoimmune disease, and allograft rejection. Method (A) provides an  
XX CC immunisation method which, unlike prior art, is not limited by the host  
XX CC immune response against viral vectors

SQ Sequence 15 AA;  
Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15  
| | | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPDQ 15

## RESULT 4

AA49659  
ID AAY49659 standard; peptide; 15 AA.

XX AAY49659;

AC 14-JAN-2000 (first entry)

DE Tumour antigenic peptide SEQ ID NO:26.

KW Human; sdh3.10; SAGE; sdp3.8; HAGE; sdp3.5; TRAP; sarcoma;  
KW tumour rejection antigen precursor; tumour associated nucleic acid;  
KW carcinoma; cancer; immune response; diagnosis.

XX Synthetic.

XX WO9953061-A2.

XX 21-OCT-1999.

XX 14-APR-1999; 99WO-US008163.

XX 15-APR-1998; 98US-0060706.

XX 27-JUL-1998; 98US-00122989.

XX 30-OCT-1998; 98US-00183706.

XX 30-OCT-1998; 98US-00183789.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Martelange V, De Smet C, Boon-Falleur T;

XX WPI; 1999-G20430/53.

XX New nucleic acid encoding sarcoma-associated gene products, useful for

XX diagnosing, e.g. treating and preventing cancer.

XX Disclosure; Page 25; 93pp; English.

XX The present invention describes sarcoma-associated gene products (I).  
XX Agents, specifically sarcoma associated nucleic acids (II) or their  
XX expression products that are tumour rejection antigens (TRA), that  
XX selectively increase formation of HLA (human leucocyte antigen)/(II)  
XX complexes are used for treating cancer, especially sarcoma and carcinoma,  
XX in humans and other animals. Compositions containing autologous cytolytic  
XX T cells (CTL), specific for the HLA/(I) complex, are similarly useful,  
XX also transformed cells that stimulate such CTL in vivo (III) are also  
XX used; (i) as source of therapeutic antisense sequences that reduce  
XX expression of (II); (ii) for recombinant production of (I); (iii)  
XX particularly its fragments, as primers and probes in usual hybridisation  
XX and amplification assays, for diagnosis, prognosis and monitoring of  
XX tumours, or for measuring binding specificity of HLA molecules or CTL  
XX clones; (iv) to identify related sequences; and (v) for generating  
XX transgenic animals, e.g. for studying cancer and immune responses to it.  
XX (I) are used to raise specific antibodies (Ab) and therapeutically. Ab  
XX are used to diagnose tumours in immunoassays, also for delivering drugs,  
XX toxins, imaging agents etc. to (I)-expressing cells. AAY49637 to AAY49670  
XX represent exemplary tumour antigenic peptides given in the present  
XX invention

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15

Db 1 DYSYLQSDPDSPDQ 15

## RESULT 5

AA491749

ID AAY01749 standard; peptide; 15 AA.

XX

AC AAY01749;

XX 25-JUN-1999 (first entry)

XX Exemplary antigenic peptide derived from Tyrosinase.

DE MAGE-3; tumour associated gene; human leucocyte antigen Class II;  
KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;  
KW osteosarcoma; leukemia; carcinoma.

XX Homo sapiens.

XX WO9914326-A1.

XX 25-MAR-1999.

XX 04-SEP-1998; 98WO-US018601.

XX 12-SEP-1997; 97US-00928615.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYVR-) UNIV VRIJE BRUSSEL.

XX Thielemans K, Heirman C, Corthals J, Chaux P, Stroobant V;

XX Boon-Falleur T, Van Der Bruggen P, Luiten R;

XX WPI; 1999-244031/20.

XX Isolated peptides that bind to human leucocyte antigen class II

XX molecules.

XX Disclosure; Page 29; 88pp; English.

XX The present sequence represents an exemplary tumour associated peptide  
XX antigen. The specification describes a MAGE-3 tumour associated gene.  
XX Peptides (AAY01721-25) that bind human leucocyte antigen (HLA) Class II  
XX molecules can be derived from the MAGE-3 protein. These peptides and  
XX autologous CD4+ cells that bind to a complex of MAGE-3 peptide and HLA  
XX Class II, are used to treat MAGE-3 related diseases, particularly cancers  
XX (e.g. melanoma, osteosarcoma, leukemia and various forms of carcinoma).  
XX The peptides are also used to produce specific antibodies. Detection of  
XX of the peptides, e.g. in binding assays, particularly with antibodies, is  
XX used for diagnosis of such diseases

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15

Db 1 DYSYLQSDPDSPDQ 15

## RESULT 6

AA491516

ID AAY71516 standard; peptide; 15 AA.

XX AAY71516;

XX 12-OCT-2000 (first entry)

XX Human Tyrosinase peptide-6.

XX Tyrosinase; human; Tumour Rejection Antigen; TRA; tumour; cancer; HLA;  
KW Human Leucocyte Antigen; MHC; Major Histocompatibility Complex; CTL;  
KW cytolytic T-lymphocyte; immune response stimulator; prophylaxis; therapy;  
KW diagnosis; TNF; tumour necrosis factor; vaccine; cytostatic.

XX Homo sapiens.

XX



PN WO200032769-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 XX 26-NOV-1999; 99WO-IB002018.  
 PF  
 XX 27-NOV-1998; 98GB-00026143.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;  
 PI WPI; 2000-412317/35.  
 DR  
 XX Novel polypeptides expressed in tumor cells useful for treating cancers  
 PT have an ability to complex with a major histocompatibility complex  
 PT molecule and comprises a specific unbroken amino acid sequence.  
 PT  
 XX Disclosure; Page 19; 80pp; English.  
 PS  
 XX The patent discloses WAGE-A10 and WAGE-A8 polypeptide, nonapeptide and  
 CC decapeptide sequences, that function as tumour rejection antigens (TRAs).  
 CC These peptides are capable of forming a complex with major  
 CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte  
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune  
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune  
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,  
 CC therapy and diagnosis of tumours and are effective in controlling or  
 CC preventing tumour growth. The present sequence is the human tyrosinase  
 CC peptide-6, that corresponds to residues 448-462 of the tumour associated  
 CC gene, tyrosinase encoding protein. It can be administered to induce or  
 CC enhance an immune response and is presented by HLA-DR4 complex. This  
 CC peptide can serve as a tumour rejection antigen (TRA) and in combination  
 CC with adjuvants, can produce vaccines useful for treating a variety of  
 CC tumours  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDPSFQD 15  
 |||||  
 DB 1 DYSYLQSDPDPSFQD 15  
 |||||  
 RESULT 7  
 AAY90800  
 ID AAY90800 standard; peptide; 15 AA.  
 XX  
 AC AAY90800;  
 XX  
 DT 25-AUG-2000 (first entry)  
 XX  
 DE Human leukocyte antigen DR4 peptide SEQ ID NO:29.  
 XX  
 KW Human leukocyte antigen; HLA-B35; binding; recognition; lysis;  
 KW cytolytic T cell; tyrosinase; immune response; diagnosis; identification;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200021551-A1.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 04-OCT-1999; 99WO-US023038.  
 XX  
 PR 09-OCT-1998; 98US-00169717.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX

PI Ooms A, De Giovanni G, Morel S, Van Den Eynde B, Boon-Falleur T;  
 WPI; 2000-317842/27.  
 DR  
 XX Isolated peptides, sometimes derived from tyrosinase, which bind to HLA-  
 PT B35 leading to recognition and lysis of the resulting complexes by  
 PT cytolytic T cells.  
 XX  
 PS Example 3; Page 9; 20pp; English.  
 XX  
 CC The present invention describes isolated peptides which bind to human  
 CC leukocyte antigen (HLA)-B35 molecules leading to recognition and lysis of  
 CC the resulting complexes by cytolytic T cells. The isolated peptides are  
 CC sometimes derived from tyrosinase. Compositions comprising the peptides  
 CC of the invention can be used to generate immune responses, preferably in  
 CC humans, but also in non-human animals to generate immune components  
 CC which can then be used to treat humans or diagnostically.  
 CC Therapeutically, the peptides are useful in generation of cytolytic T  
 CC cells either in vitro or in vivo which specifically lyse pathogenic  
 CC cells. The peptides can also be used to identify HLA-B35 positive cells,  
 CC or to remove HLA-B25 positive cells from mixtures containing such cells.  
 CC Nucleic acid molecules encoding the peptides can be used inter alia as  
 CC probes to identify cells which are expressing tyrosinase. The present  
 CC sequence represents an HLA binding peptide used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDPSFQD 15  
 |||||  
 DB 1 DYSYLQSDPDPSFQD 15  
 |||||  
 RESULT 8  
 AAB23672  
 ID AAB23672 standard; peptide; 15 AA.  
 XX  
 AC AAB23672;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:24.  
 XX  
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytostatic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200049041-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-JP000941.  
 XX  
 PR 19-FEB-1999; 99JP-00041535.  
 XX  
 PA (SUME) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Udono H, Yui K;  
 XX WPI; 2000-543748/49.  
 DR  
 XX Fused protein capable of inducing cellular immune response, useful as  
 PT active ingredient for drug compositions in preventing and/or treating  
 PT infectious diseases such as malaria or cancer.  
 PT  
 PS Claim 7; Page 57; 72pp; Japanese.

XX The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ARAse domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (I) has cytostatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed CTL epitope for  
 CC use in a fused protein of the present invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDPSFQD 15  
 DB 1 DYSYLQSDPDPSFQD 15  
 RESULT 9  
 AAY92296  
 ID AAY92296 standard; peptide; 15 AA.  
 AC AAY92296;  
 DT 10-AUG-2000 (first entry)  
 DE Tyrosinase antigenic peptide epitope (residues 448-462).  
 XX Tyrosinase; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;  
 KW human leukocyte antigen; HLA.  
 KW Homo sapiens.  
 XX WO200020445-A2.  
 FN 13-APR-2000.  
 PD 15-SEP-1999; 99WO-IB001664.  
 PF 02-OCT-1998; 98US-00165863.  
 PR 09-APR-1999; 99US-00289350.  
 XX (CHAU/) CHAUX P.  
 PA (LUIT/) LUITEN R.  
 PA (DEMO/) DEMOTTE N.  
 PA (DUFF/) DUFFOUR M.  
 PA (LURQ/) LURQUIN C.  
 PA (TRAV/) TRAVERSARI C.  
 PA (STRO/) STROOBANT V.  
 PA (CORN/) CORNELIS G R.  
 PA (BOON/) BOON-FALLEUR T.  
 PA (VBRU/) VAN DER BRUGGEN P.  
 PA (SCHU/) SCHULTZ E.  
 PA (WARN/) WARNIER G.  
 XX Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;  
 PI Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;  
 PI Schult E, Warnier G;  
 XX WPI; 2000-303739/26.  
 XX Isolation of cytotoxic T-lymphocytes clones by successive steps of  
 PT stimulation and testing of lymphocytes with antigen presenting cells  
 PT which present antigens derived from different expression systems.  
 XX

PS Disclosure; Page 22; 99pp; English.  
 XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones  
 CC comprises successive steps of stimulation and testing of lymphocytes with  
 CC antigen presenting cells (APCs) which present antigens derived from  
 CC different expression systems. The CTL clones isolated recognize specific  
 CC antigenic peptides of proteins, preferably of the MAGE family. The APC is  
 CC autologous and each expression systems is different from at least one of  
 CC the other expression systems, therefore isolating a cytotoxic T cell  
 CC clone specific for the protein. The method can also be used to identify  
 CC an antigenic peptide epitope. Isolated CTL clones specific for a  
 CC peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells  
 CC specific for the complexes, peptides or cells which present the complexes  
 CC on the cell surface are useful for treating pathological conditions  
 CC characterized by abnormal expression of the complexes  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDPSFQD 15  
 DB 1 DYSYLQSDPDPSFQD 15  
 RESULT 10  
 AAY56611  
 ID AAY56611 standard; peptide; 15 AA.  
 AC AAY56611;  
 DT 21-FEB-2000 (first entry)  
 DE Tyrosinase gene MHC molecule HLA-DR4 peptide SEQ ID NO:27.  
 KW HLA-A\*0201; human leukocyte antigen; cytolytic T cell; CTL; tumour;  
 KW Melan-A; peripheral blood lymphocyte; pBL; immune complex; melanoma;  
 KW MHC molecule; beta2-microglobulin; cytotoxic T lymphocyte; vaccine;  
 KW immune response; cancer; tyrosinase; tumour rejection antigen;  
 KW major histocompatibility complex.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO950637-A2.  
 FN 07-OCT-1999.  
 PD 25-MAR-1999; 99WO-US006615.  
 PF 27-MAR-1998; 98US-00049850.  
 PR (LUDW-) LUDWIG INST CANCER RES.  
 PA (UYOX-) UNIV OXFORD.  
 XX Romero P, Dunbar R, Valmori D, Ogg G, Cerrotini J, Cerundolo V;  
 PI Pittet M;  
 XX WPI; 2000-052636/04.  
 XX New isolated complex of binding partners and immune complexes containing  
 PT major histocompatibility molecules and peptide, used to isolate and detect  
 PT cytotoxic T cells, particularly directed against cancer.  
 XX Example 50; Page 64; 91pp; English.  
 XX The present invention describes an isolated complex (A) comprising: (i)  
 CC first and second binding partners (BP1, BP2); and (ii) several immune  
 CC complexes (IC) containing a major histocompatibility complex (MHC)  
 CC molecule (I), a beta2-microglobulin molecule (b2MG) and a peptide (II)  
 CC that binds specifically to (I). (A) are used for analysis of cytolytic T

CC cells (CTL) for characterisation of an immune response to tumours or for  
CC monitoring vaccine trials. Particularly they are used to isolate or  
CC detect particular CTL (especially those in tumour-infiltrated lymph  
CC nodes), including visualisation of antigen-specific CTL and determination  
CC if the cells have been activated by in vivo exposure to antigen. Isolated  
CC precursor cells may be expanded in vitro to produce cells with high  
CC tumoricidal activity, for therapeutic or diagnostic use. A method from  
CC the present invention allows: (i) preselection of T cell clones for use  
CC in immunotherapy according to their homing molecules; and (ii) improves  
CC the lytic activity of T cells populations by inhibition of natural killer  
CC cell receptors. The present sequence represents a peptide used in the  
CC exemplification of the present invention

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
| | | | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 11

AY84292  
ID AAY84292 standard; peptide; 15 AA.

XX AC AAY84292;

XX DT 12-JUL-2000 (first entry)

XX DE Tumour associated antigen derived from tyrosinase.

XX KW tumour rejection antigen; macrophage colony stimulating gene;  
KW macrophage-colony stimulating factor; antigen presenting cell;  
KW human leukocyte antigen; CD8+ cytotoxic T lymphocyte.

XX OS Homo sapiens.

XX PN WO200013699-A1.

XX PD 16-MAR-2000.

XX PF 03-SEP-1999; 99WO-US020344.

XX PR 04-SEP-1998; 98US-0099077P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Probst-Kepper M, Van Den Eynde B, Boon-Falleur T;

XX WPI; 2000-256859/22.

XX Isolated polypeptide used to treat subjects having a disorder  
PT characterized by expression of alternative open reading frame macrophage-  
PT colony stimulating factor comprises 25 amino acid residue sequence.

XX Disclosure; Page 21; 74pp; English.

XX AAY84270-Y84303 represent peptides which are tumour associated antigens.  
CC They can be administered in conjunction with the tumour rejection antigen  
CC precursor of the invention to induce anti-tumour responses. The tumour  
CC rejection antigen precursor of the invention is encoded by an alternative  
CC open reading frame (ORF) of human macrophage colony stimulating gene.  
CC Peptides derived from the alternative ORF of macrophage-colony  
CC stimulating factor, when presented by an antigen presenting cell having a  
CC human leukocyte antigen (HLA) class I molecule, effectively induce the  
CC activation and proliferation of CD8+ cytotoxic T lymphocytes. Polypeptide  
CC and nucleic acids derived from the alternate ORF of macrophage-colony  
CC stimulating factor are useful for enriching selectively a population of T  
CC lymphocytes with CD8+ T lymphocytes. They are also useful for diagnosing  
CC a disorder characterized by expression of the polypeptide, and for

CC identifying functional variants and mimetics

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
| | | | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 12

AY82975  
ID AAY82975 standard; peptide; 15 AA.

XX AC AAY82975;

XX DT 19-JUN-2000 (first entry)

XX DE Tyrosinase tumour associated antigen.

XX KW Tumour; tumour associated antigen; retrovirus; antisense; treatment;  
KW probe; primer; HLA; cytotoxic T-lymphocyte; cancer; testis; antibody;  
KW CTL; helper T-lymphocyte; MAGE; RAGE; GAGE; Gnt-V; MUM; CDK4;  
KW beta catenin; tyrosinase; Melan-A; gp100; PRAME.

XX OS Homo sapiens.

XX PN WO200006598-A1.

XX PD 10-FEB-2000.

XX PF 15-JUL-1999; 99WO-US016236.

XX PR 29-JUL-1998; 98US-00124398.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Coulie P, Boon-Falleur T;

XX WPI; 2000-205453/18.

XX Novel nucleic acids encoding melanoma associated gene products and their  
PT fragments and variants, useful for treating endogenous retrovirus  
PT mediated tumors, especially melanomas.

XX Disclosure; Page 26; 77pp; English.

XX Tumor associated disorders (e.g. endogenous retrovirus mediated tumors,  
CC especially melanomas) can be treated or ameliorated by administering  
CC antisense nucleic acid to reduce the expression of tumour associated  
CC genes such as HERV-AVL3-B. Progression of a disorder characterized by the  
CC expression of the HERV-AVL3-B endogenous retrovirus tumor rejection  
CC antigen (ERTRA) can be diagnosed or monitored by contacting a non-testis  
CC biological sample with an agent that binds to the complex and determining  
CC the interaction. A disorder can also be treated by administering an agent  
CC that enriches the presence of HLA and HERV-AVL3-B ERTRA or by  
CC administering autologous cytotoxic T-cells sufficient to ameliorate the  
CC disorder. Fragments of the HERV-AVL3-B coding sequence are useful as  
CC probes or amplification primers for determining the expression of HERV-  
CC AVL3-B genes, to express tumor associated polypeptides in vivo and in  
CC vitro and to prepare fragments of such polypeptides to synthesize  
CC antibodies. Antigenic peptides of HERV-AVL3-B can be useful for  
CC generating antibodies either alone or as fusion proteins, as components  
CC of immunoassay and for determining the binding specificity of HLA  
CC molecules and/or cytotoxic T lymphocyte (CTL) for HERV-AVL3-B proteins.  
CC Peptides derived from the HERV-AVL3-B coding sequence and which are  
CC presented by MHC molecules and recognised by CTL or helper T-lymphocytes  
CC can be combined with peptides from other tumour rejection antigens by  
CC preparation of hybrid nucleic acids or polypeptides to produce polytopes.  
CC This exemplary tumour associated peptide antigen corresponds to amino

CC acids 448-462 of the tyrosinase polypeptide. See also AAY82953-Y82986

XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15  
| | | | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPDQ 15

## RESULT 13

AA02618  
ID AAB02618 standard; peptide; 15 AA.

XX AC AAB02618;

XX DT 18-AUG-2000 (first entry)

XX DE Tumour associated peptide antigen from Tyrosinase #7.

XX KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;  
KW cancer; human; tumour; tumour associated gene product.

XX OS Homo sapiens.

XX PN WO200020581-A1.

XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-US021230.

XX PR 05-OCT-1998; 98US-00166448.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI (UYVR-) UNIV VRIJE BRUSSEL.

XX PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;  
PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;  
PI Heirman C;

XX WPI; 2000-317713/27.

XX PT New MAGE-A3 class II binding peptides, useful to diagnose and treat  
PT tumors, are fragments of MAGE-A3 which bind to and are presented to T  
PT lymphocytes by human leukocyte antigen class II molecules.  
PS Disclosure; Page 33; 119pp; English.

CC The present invention relates to MAGE-A3 (tumour associated gene product)  
CC human leukocyte antigen (HLA) class II-binding peptides (see AAB02566-  
CC B02595, and AAB02633-B02637). These peptides are presented to T cells in  
CC the context of HLA class II molecules. The peptides stimulate the  
CC activity and proliferation of CD4+ T lymphocytes. The invention also  
CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928 and  
CC AAA37938-A37940). The peptides and nucleotide sequences can be used to  
CC create antibodies against the MAGE-A3 peptides, the antibodies, peptides  
CC and nucleotide sequences can be used to create a vaccine. The peptides  
CC are used to diagnose or treat a disorder characterized by expression of  
CC MAGE-3, particularly cancer. The methods can also be used in the  
CC diagnosis of disorders associated with MAGE-3 expression. Included in the  
CC invention are other human tumour antigens (see AAB02596-B02637), and PCR  
CC primers used in the course of the invention (see AAA37929-A37937 and  
CC AAA37941-A37942)

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15  
| | | | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPDQ 15

## RESULT 14

AA08690  
ID AAB08690 standard; peptide; 15 AA.

XX AC AAB08690;

XX DT 02-JAN-2001 (first entry)

XX DE Antigenic peptide from tumour rejection antigen tyrosinase.

XX KW Epha3; HLA class II-binding peptide; human leukocyte antigen; antigen;  
KW CD4+ T lymphocyte; tumour associated gene; vaccine.

XX OS Homo sapiens.

XX PN WO200050589-A1.

XX PD 31-AUG-2000.

XX PF 18-FEB-2000; 2000WO-US004326.

XX PR 22-FEB-1999; 99US-0121170P.

XX PR 08-OCT-1999; 99US-0158566P.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chiari R, Coulie P, Boon-Falleur T;

XX WPI; 2000-572089/53.

XX PT Novel tyrosine kinase receptor, Epha3 human leukocyte antigen (HLA) class  
PT II binding peptide and nucleic acid encoding the receptor, useful for  
PT diagnosing and treating conditions characterized by expression of Epha3  
PT gene.  
PS Disclosure; Page 35; 107pp; English.

CC AAB08668-B08704 represent antigenic peptides characteristic of tumours.  
CC The peptides may be combined in vaccines with a human Epha3 HLA (human  
CC leukocyte antigen) class II-binding peptide. Epha3 antigens, when  
CC presented by an antigen presenting cell having a HLA class II molecule,  
CC effectively induce activation and proliferation of CD4+ T lymphocytes.  
CC Epha3 is a tumour associated gene. Epha3 HLA binding peptides are used  
CC for selectively enriching a population of T lymphocytes. The peptides are  
CC also used for diagnosing a disorder characterized by Epha3 or Epha3 HLA  
CC binding peptide expression. The peptides are also used to treat a  
CC disorder characterized by Epha3 expression. The Epha3 binding peptides  
CC are useful in producing vaccines and antibody

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15  
| | | | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPDQ 15

## RESULT 15

AA02107  
ID AAE02107 standard; peptide; 15 AA.

XX AC AAE02107;

XX DT 31-JUL-2001 (first entry)

XX XX



PR 25-OCT-2000; 2000US-0243212P.  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA  
PI Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;  
XX Demotte N, Schultz E;  
XX WPI; 2001-488724/53.  
XX Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or HLA-B44  
PT Binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used in  
PT diagnosis and treatment of a disorder characterized by expression of MAGE  
PT -A1 or -A3.  
XX  
XX Disclosure; Page 28; 103pp; English.  
XX  
XX The invention relates to functional variants and isolated mimetics of a  
CC MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide, or  
CC of a MAGE-A3 HLA-B35 binding peptide, identified by methods described in  
CC the specification. MAGE genes encode tumour rejection antigens (TRAs)  
CC presented to T lymphocytes by HLA-B35 and HLA-B44 molecules. The MAGE  
CC antigenic peptide acts by binding to HLA molecules on tumour cells and  
CC stimulating recognition of these cells and thus signalling them to the  
CC immune system for destruction. The peptide when presented by HLA molecule  
CC induces the activation and stimulation of CD8+ cytotoxic T lymphocytes.  
CC The MAGE antigenic peptide is used to treat and diagnose disorders  
CC characterised by expression of MAGE-A1 or -A3. Disorders include cancers  
CC e.g. melanomas, oesophageal, lung, head and neck, breast, colorectal,  
CC prostate, renal, bladder, hepatocellular, papillary thyroid and gastric  
CC carcinomas, myelomas, brain tumours, sarcomas, seminomas, and ovarian  
CC tumours. The present sequence is human tyrosinase tumour associated  
CC antigenic peptide presented by major histocompatibility complex (MHC) HLA  
CC -DR4. The antigenic peptide is used in combination with peptides of the  
CC invention for inducing an immune response  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYSYLQSDPDSPDQ 15  
Db 1 DYSYLQSDPDSPDQ 15  
RESULT 18  
ABG79140  
ID ABG79140 standard; peptide; 15 AA.  
XX  
XX ABG79140;  
XX  
XX 15-NOV-2002 (first entry)  
XX  
XX Human tyrosinase class II HLA tumour-restricted antigen peptide #2.  
XX  
XX Cell penetrating peptide; cancer; melanoma; thymoma; antigen;  
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;  
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;  
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;  
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;  
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;  
KW cytostatic; human.  
XX  
XX Homo sapiens.  
OS  
XX WO200264057-A2.  
XX  
XX 22-AUG-2002.  
XX  
XX 15-FEB-2002; 2002WO-US005212.  
XX  
XX 15-FEB-2001; 2001US-0268687P.

XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA  
XX Wang R;  
PI  
XX WPI; 2002-627577/67.  
XX  
XX Novel composition for treating a disease in an animal, comprises an  
PT immune effector cell and cell penetrating peptide associated with an  
PT antigen or antibody.  
XX  
XX Disclosure; Page 22; 61pp; English.  
XX  
XX The invention relates to a composition (I) comprising an immune effector  
CC cell and a cell penetrating peptide (CPP) associated with an antigen or  
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated  
CC with an antigen, and a pharmaceutically acceptable carrier and (2)  
CC preparing a composition for a disease, by providing (I) and CPP  
CC associated with an antigen for disease, and introducing the antigen-  
CC associated CPP to (I), where antigen enters into the cell. The antigens  
CC are, for example, tumour antigen derived epitopes recognised by tumour  
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I  
CC or II. The composition is useful for enhancing immunity in an animal to a  
CC disease, by administering a mature dendritic cell comprising CPP  
CC associated with an antigen to disease, to the animal, such that following  
CC the administration, animal is protected from disease, where the animal  
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a  
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung  
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine  
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,  
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).  
CC The animal is further subjected to a cancer treatment including surgery,  
CC radiation, chemotherapy or gene therapy. The administration of (I),  
CC preferably dendritic cell is prior to, subsequent to or concurrent with,  
CC the cancer treatment. The present sequence is a tumour antigen derived  
CC epitope for inclusion in the composition of the invention  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 100.0%; Score 83; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYSYLQSDPDSPDQ 15  
Db 1 DYSYLQSDPDSPDQ 15  
RESULT 19  
ADA19544  
ID ADA19544 standard; peptide; 15 AA.  
XX  
XX ADA19544;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human cancer antigen, tyrosinase (MHC HLA-DR4) #2.  
XX  
XX Lymphoid tissue-specific cell; haematopoietic progenitor cell;  
KW lymphoreticular stromal cell; transplantation; implantation;  
KW autoimmune disease; infectious disease; maintenance; expansion;  
KW differentiation; T cell tolerance; immune tolerance; T-cell reactivity;  
KW therapeutic; differentiated progeny; antigen; MHC;  
KW major histocompatibility complex; cancer; human.  
XX  
XX Homo sapiens.  
OS  
XX US6548299-B1.  
XX  
XX 15-APR-2003.  
XX  
XX 18-MAY-2000; 2000US-00574749.  
XX

PR 12-NOV-1999; 99WO-US026795.

XX (PYKE/) PYKETT M J;  
 PA (ROSE/) ROSENZWEIG M.  
 PA (SCAD/) SCADDEN D T.  
 PA (POZN/) POZNANSKY M C.

XX Pykett MJ, Rosenzweig M, Scadden DT, Poznansky MC;  
 XX WPI; 2003-605374/57.

XX Producing lymphoid tissue-specific cell in vivo, useful in  
 PT transplantation, implantation, autoimmune and/or infectious diseases by  
 PT introducing hematopoietic progenitor and lymphoreticular stromal cells  
 PT into a porous solid matrix.

XX Disclosure; SEQ ID NO 25; 34pp; English.

XX The invention discloses a method for producing lymphoid tissue-specific  
 CC cell in vivo, comprising introducing hematopoietic progenitor cells and  
 CC lymphoreticular stromal cells into a porous, solid matrix having  
 CC interconnected pores of a pore size sufficient to permit the cells to  
 CC grow throughout the matrix, and co-culturing the hematopoietic  
 CC progenitor cells and lymphoreticular stromal cells. The methods are  
 CC useful in transplantation, implantation, autoimmune diseases and/or  
 CC infectious diseases. They are particularly useful for in vivo  
 CC maintenance, expansion and/or differentiation of hematopoietic  
 CC progenitor cells, for inducing T cell tolerance, for treating a subject  
 CC to enhance immune tolerance, for inducing T cell reactivity, and for  
 CC identifying an agent suspected of affecting hematopoietic cell  
 CC development. The lymphoid tissue-specific cells are useful in laboratory  
 CC analysis and in therapeutics. The method provides rapid generation of a  
 CC large number of differentiated progeny. The sequence presented is a  
 CC cancer antigen which was used in the invention to expand hematopoietic  
 CC progenitor cells.

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
 |||||  
 Db 1 DYSYLQSDPDPSFQD 15

RESULT 20  
 AAU84918  
 ID AAU84918 standard; peptide; 30 AA.

XX AAU84918;

DT 08-MAY-2002 (first entry)

DE Human Tyros segment 30.

XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
 KW viral infection; human immunodeficiency virus; melanoma;  
 KW bacterial infection; Salmonella; Legionella; parasitic infection;  
 KW Trypanosoma; Toxoplasma; Giardia.

XX Homo sapiens.

XX WO200190197-A1.

XX 29-NOV-2001.

XX 25-MAY-2001; 2001WO-AU000622.

XX 26-MAY-2000; 2000AU-00007761.

XX (AUSU ) UNIV AUSTRALIAN NAT.

XX Thomson SA, Ramshaw IA;  
 XX WPI; 2002-147575/19.

XX N-PsDB; ABK36738.

XX New synthetic polypeptides having several different segments of at least  
 PT one parent polypeptide linked together differently compared to the  
 PT linkage in the parent polypeptide, for inducing immune response against a  
 PT pathogen or cancer.

XX Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising  
 CC several different segments of at least one parent polypeptide linked  
 CC together in a different relationship relative to their linkage in the  
 CC parent polypeptide to impede, abrogate or otherwise alter at least one  
 CC function associated with the parent polypeptide and for inducing an  
 CC immune response against a pathogen or cancer. Also included are a  
 CC synthetic polynucleotide encoding and a computer system for designing the  
 CC synthetic polypeptides. The synthetic polypeptides and polynucleotides  
 CC are referred to as a Savine. The synthetic polypeptide is useful for  
 CC modulating immune responses preferably directed against a pathogen or a  
 CC cancer, (e.g., cancers of the lung, breast, ovary, kidney, bone liver,  
 CC and neck, pancreas, prostate, stomach, bladder, kidney, colon, head  
 CC oesophagus, brain, testicle, uterus), as potentiating agents.  
 CC Compositions comprising the polypeptide may be used in the treatment or  
 CC prophylaxis against viral (such as infections caused by HIV (human  
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic  
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is  
 CC a peptide derived from a parent protein used to construct a savine of the  
 CC invention

XX Sequence 30 AA;

Query Match 100.0%; Score 83; DB 5; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
 |||||  
 Db 15 DYSYLQSDPDPSFQD 29

RESULT 21  
 AAU38167  
 ID AAU38167 standard; protein; 508 AA.

XX AAU38167;

XX 13-MAR-1998 (first entry)

XX Mutant human tyrosinase (Pmel134A).

XX Pmel17; lambda mel.17-1, ATCC 40264; melanisation; human; melanin;  
 KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;  
 KW tyrosinase; Pmel134A; mutant.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..18

FT Peptide /label= sig\_peptide

FT Peptide 19..508

XX /label= mat\_peptide

XX US5679511-A.

XX 21-OCT-1997.

XX PF 01-JUN-1992; 92US-00891942.  
 XX PR 06-OCT-1986; 86US-00915753.  
 XX PR 07-JUN-1989; 89US-00362847.  
 XX (GUTH-) GUTHRIE FOUND MEDICAL RES INC DONALD.  
 XX PA (INDV) UNIV INDIANA FOUND.  
 XX PI Kwon BS;  
 XX DR WPI; 1997-525715/48.  
 XX DR N-PSDB; AAT95734.  
 XX PT Lambda mel 17-1 cDNA and Emell17 protein - useful as melanin biosynthesis probe.  
 XX PS Disclosure; Col 67-72; 67pp; English.  
 XX CC The present sequence is disclosed in the specification, which describes the isolation of Emell17, a protein encoded by cDNA isolated from lambda mel 17-1 (ATCC 40264). The degree of melanisation in a human melanocyte can be determined by subjecting human melanocyte RNA to a Northern blot analysis, using the cDNA as a probe  
 XX SQ Sequence 508 AA;  
 Query Match 100.0%; Score 83; DB 2; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDSFQD 15  
 DB 448 DYSYLQSDPDSFQD 462  
 |||||  
 RESULT 22  
 AAR56309  
 ID AAR56309 standard; protein; 529 AA.  
 XX AC AAR56309;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 19-MAR-1995 (first entry)  
 XX DE Human tyrosinase acting as tumor rejection antigen precursor.  
 XX KW Tyrosinase; enzyme; tumor rejection antigen precursor; HLA;  
 XX KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT Peptide 1..10  
 XX PN WO9414459-A1.  
 XX PD 07-JUL-1994.  
 XX PF 14-DEC-1993; 93WO-US012200.  
 XX PR 22-DEC-1992; 92US-00994928.  
 XX PR 28-APR-1993; 93US-00054714.  
 XX PR 23-JUN-1993; 93US-00081673.  
 XX PA (LUDW-) LUDWIG INST CANCER RES.  
 XX PI Boon-Falleur T, Brichard V, Van Pel A, De Plaen E, Coullie P;  
 XX PI Renaud J, Wolfel T, Lethe B;  
 XX WPI; 1994-234342/28.  
 XX DR N-PSDB; AAO66548.

PT Method for the identification of HLA complexes - used for the detection of abnormal cells.  
 XX PS Disclosure; Page 19; 3lpp; English.  
 XX CC This normally occurring tyrosinase which may act as a tumor rejection antigen precursor and be processed to form a peptide tumor rejection antigen (AAR56310) which is presented on the surface of a cell, in combination with HLA-A2, thereby stimulating lysis of cytotoxic T-lymphocyte clones. (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 529 AA;  
 Query Match 100.0%; Score 83; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDSFQD 15  
 DB 448 DYSYLQSDPDSFQD 462  
 |||||  
 RESULT 23  
 AAR63623  
 ID AAR63623 standard; protein; 529 AA.  
 XX AC AAR63623;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 21-JUN-1995 (first entry)  
 XX DE Human tyrosinase protein.  
 XX KW Human; tyrosinase; compound; hair; follicle; liposome; lipophilic;  
 XX KW lipophobic; stratum corneum; melanin; hair dye; glycoprotein; alopecia;  
 XX KW chemotherapy; transforming growth factor; growth stimulant; aromatase;  
 XX KW cyclosporin A; macromolecule; polymer.  
 XX OS Homo sapiens.  
 XX PN WO9422468-A1.  
 XX PD 13-OCT-1994.  
 XX PF 01-APR-1994; 94WO-US003634.  
 XX PR 02-APR-1993; 93US-00041553.  
 XX PR 13-JAN-1994; 94US-00181471.  
 XX PA (ANTI-) ANTICANCER INC.  
 XX PI Li L, Lishko VK;  
 XX DR WPI; 1994-332816/41.  
 XX DR N-PSDB; AAO72871.  
 XX PT Liposomes for delivering protein, nucleic acid etc. to hair follicles - e.g. to restore hair colour, prevent hair loss during chemotherapy, stimulate hair growth etc.  
 XX PS Claim 6; Page 67-70; 100pp; English.  
 XX CC The amino acid sequence of a human tyrosinase protein. This is an example of a compound which can be delivered to hair follicles via a novel liposome composition. The liposomes are comprised of a lipophilic or lipophobic compound which will selectively target the hair follicle (via the stratum corneum) without damaging or unwanted effects on cells outside the follicle. Compounds e.g. tyrosinase (or the DNA encoding it), melanin or hair dyes, can be delivered to the hair follicle to restore hair colour or condition. Other compounds targeted at hair follicles can include: p-glycoprotein (AAQ72872) (for treatment of chemotherapy-induced alopecia); human transforming growth factor alpha (AAQ72873) (for reversal of wavy hair); hair growth stimulants (e.g. cyclosporin A or aromatase)



CC or antisense sequences. The methods allows compounds (e.g. macromolecules  
CC or polymers), which would not normally reach the hair follicles, to be  
CC delivered to these target areas. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
CX  
XX  
SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPQD 15  
|||||  
Db 448 DYSYLQSDPDSPQD 462

RESULT 24  
AAW00184  
ID AAW00184 standard; protein; 529 AA.

XX AC AAW00184;  
XX DT 18-OCT-1996 (first entry)  
XX DE Human tyrosinase.  
XX KW Human; tyrosinase; detection; primer; reverse transcription; amplify;  
XX KW transcription region; detection.  
XX OS Homo sapiens.  
XX PN JP08140699-A.  
XX PD 04-JUN-1996.  
XX PF 22-NOV-1994; 94JP-00288041.  
XX PR 22-NOV-1994; 94JP-00288041.  
XX PA (PORK ) POLA CHEM IND INC.  
XX DR WPI; 1996-316329/32.  
XX DR N-PSDB; AAT33316.  
XX PT Detection of tyrosinase mRNA - by amplification of tyrosinase mRNA allows  
XX accurate detection of trace amounts of RNA.  
XX PS Disclosure; Page 7-9; 10pp; Japanese.

XX CC This sequence represents human tyrosinase. The cDNA encoding this  
XX sequence was detected by the method of the invention using the primers  
XX given in AAT33317-24. The method comprises synthesising tyrosinase cDNA  
XX from a sample by reverse transcription and then amplifying the cDNA using  
XX primers specific for, or complementary to, sequences within the  
XX transcription region of the tyrosinase gene. Amplification using these  
XX primers produces a competitive cDNA which can also be amplified. This  
XX method can be used to specifically detect trace amounts of human  
XX tyrosinase mRNA  
XX  
SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPQD 15  
|||||  
Db 448 DYSYLQSDPDSPQD 462

RESULT 25  
AAW03306  
ID AAW03306 standard; protein; 529 AA.

XX AAW03306;  
XX AC  
XX DT 22-OCT-1996 (first entry)  
XX DE Tyrosinase melanoma antigen.  
XX KW Melanoma; tyrosinase; immunogen; vaccine; cancer; immunotherapy;  
XX transgenic animal.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Peptide 206..215  
XX FT /note= "immunogenic peptide"  
XX FT Peptide 206..214  
XX FT /note= "immunogenic peptide"  
XX PN W09621734-A2.  
XX PD 18-JUL-1996.  
XX PF 11-JAN-1996; 96WO-US000473.  
XX PR 10-JAN-1995; 95US-00370909.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Robbins PF, Rosenberg SA;  
XX DR WPI; 1996-342287/34.  
XX DR N-PSDB; AAT35901.  
XX PT Nucleic acid sequence encoding p15 melanoma antigen - and immunogenic  
XX peptide(s) derived from it, useful for diagnosis, prevention or treatment  
XX of melanoma.  
XX PS Disclosure; Page 77-79; 98pp; English.  
XX CC A DNA fragment (AAT35901) codes for tyrosinase (AAW03306), an enzyme  
XX involved in melanin synthesis. The tyrosinase was recognised by HLA-A24  
XX restricted tumour infiltrating lymphocytes from a melanoma patient.  
XX CC Tyrosinase, or its immunogenic peptides (see also AAW03304-05), can be  
XX used as a vaccine against melanoma, or to raise antibodies useful for the  
XX diagnosis, assessment or prognosis of melanoma  
XX  
SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPQD 15  
|||||  
Db 448 DYSYLQSDPDSPQD 462

RESULT 26  
AAW38166  
ID AAW38166 standard; protein; 529 AA.

XX AC AAW38166;  
XX DT 13-MAR-1998 (first entry)  
XX DE Normal human tyrosinase (Pmel134A).  
XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;  
XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;  
XX tyrosinase; Pmel134A.  
XX OS Homo sapiens.  
XX

FH Key Location/Qualifiers  
 FT Peptide 1. .18  
 FT /label= sig\_peptide  
 FT Peptide 19. 529  
 FT /label= mat\_peptide  
 XX US5679511-A.  
 PN  
 XX 21-OCT-1997.  
 XX  
 XX 01-JUN-1992; 92US-00891942.  
 XX  
 XX 06-OCT-1986; 86US-00915753.  
 XX 07-JUN-1989; 89US-00362847.  
 XX  
 XX (GUTH-) GUTHRIE FOUND MEDICAL RES INC DONALD.  
 XX (INDV ) UNIV INDIANA FOUND.  
 XX  
 XX Kwon BS;  
 XX  
 XX WPI; 1997-525715/48.  
 DR N-PSDB; AAT95733.  
 DR  
 XX Lambda mel 17-1 cDNA and Pmel17 protein - useful as melanin biosynthesis probe.  
 FT  
 XX Disclosure; Col 59-64; 67pp; English.  
 XX  
 XX The present sequence is disclosed in the specification, which describes the isolation of Pmel17, a protein encoded by cDNA isolated from lambda mel 17-1 (ATCC 40264). The degree of melanisation in a human melanocyte can be determined by subjecting human melanocyte RNA to a Northern blot analysis, using the cDNA as a probe  
 XX  
 XX Sequence 529 AA;  
 SQ  
 Query Match 100.0%; Score 83; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDSPDQD 15  
 Db 448 DYSYLQSDPDSPDQD 462  
 RESULT 27  
 AAW36519  
 ID AAW36519 standard; protein; 529 AA.  
 XX  
 XX AAW36519;  
 AC  
 XX 08-APR-1998 (first entry)  
 DT  
 XX Tyrosinase containing human leukocyte antigen-A1 epitope.  
 DE  
 XX Melanoma; immunogen; cytotoxic T lymphocyte; CTL;  
 XX human leukocyte antigen-A1; HLA-A1; human leukocyte antigen-A3; HLA-A3;  
 KW epitope; pMEL-17; tyrosinase; vaccine; protection.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH 243. .251  
 FT Region /note= "human leukocyte antigen-A1 epitope"  
 FT  
 XX W09734613-A1.  
 PN  
 XX 25-SEP-1997.  
 PD  
 XX  
 XX 17-MAR-1997; 97WO-US004958.  
 XX  
 XX 19-MAR-1996; 96US-0013972P.  
 XX 04-OCT-1996; 96US-0027627P.  
 PR

XX (UYVI-) UNIV VIRGINIA PATENT FOUND.  
 PA  
 XX Slingluff CL, Hunt DF, Shabanowitz J, Cox AL, Engelhard VH;  
 PI Kittlesen D, Skipper J, Hendrikson RC;  
 XX  
 XX WPI; 1997-479982/44.  
 DR  
 XX Melanoma-specific immunogens of pMEL-17 and tyrosinase - useful in vaccination for producing melanoma-specific cytotoxic T lymphocytes.  
 PT  
 XX Disclosure; Fig 10; 106pp; English.  
 PS  
 XX A novel melanoma specific immunogen comprises at least 1 melanoma specific cytotoxic T lymphocyte (CTL) epitope, where at least 1 of the epitopes is substantially homologous to a human leukocyte antigen-A1 (HLA-A1) and HLA-A3 restricted epitope of a melanoma antigen, either pMEL-17 or tyrosinase, i.e. the present sequence. The immunogen can be used in vaccines for protection against melanoma in mammals  
 CC  
 XX Sequence 529 AA;  
 SQ  
 Query Match 100.0%; Score 83; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDSPDQD 15  
 Db 448 DYSYLQSDPDSPDQD 462  
 RESULT 28  
 AAW71234  
 ID AAW71234 standard; protein; 529 AA.  
 XX  
 XX AAW71234;  
 AC  
 XX 16-NOV-1998 (first entry)  
 DT  
 XX Tyrosinase.  
 DE  
 XX Tyrosinase; tyrosinase cytotoxic lymphocyte response;  
 XX cytotoxic T lymphocyte; cysteine-depleted; melanoma.  
 KW  
 XX Synthetic.  
 OS  
 XX W09833810-A2.  
 PN  
 XX 06-AUG-1998.  
 PD  
 XX 29-JAN-1998; 98WO-US001592.  
 PF  
 XX 30-JAN-1997; 97US-0037781P.  
 PR  
 XX (UYVI-) UNIV VIRGINIA PATENT FOUND.  
 PA  
 XX Slingluff CL, Hunt DF, Engelhard VH, Kittlesen D;  
 PI  
 XX WPI; 1998-437388/37.  
 DR  
 XX Disease specific immunogen - comprises disease specific cytotoxic T lymphocyte epitope used to elicit melanoma specific CTL response.  
 PT  
 XX Disclosure; Fig 5; 93pp; English.  
 PS  
 XX The tyrosinase is used as a template for tyrosinase cytotoxic lymphocyte response peptides. These peptides are examples of cytotoxic T lymphocyte (CTL) epitopes which are cysteine-depleted mutants of a native disease-specific CTL epitope. The cysteine-depleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The tyrosinase epitopes are melanoma-specific and can be used in a disease-specific immunogen to protect a mammal against melanoma. The peptides may also be used to screen a sample for the presence of an antigen with the

CC same epitope, or with a different cross-reactive epitope  
 XX  
 SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
 |||||  
 Db 448 DYSYLQSDPDPSFQD 462

RESULT 29  
 AAB51344  
 ID AAB51344 standard; protein; 529 AA.

XX AC AAB51344;

XX DT 09-APR-2001 (first entry)

XX DE Human tyrosinase protein sequence SEQ ID NO:4.

XX KW Human; tyrosinase; anti-gray hair agent; hair colour; hair follicle.

XX OS Homo sapiens.

XX XX JF2000300298-A.

XX PD 31-OCT-2000.

XX PF 23-APR-1999; 99JP-00117006.

XX PR 23-APR-1999; 99JP-00117006.

XX PA (SHIS ) SHISEIDO CO LTD.

XX XX WPI; 2001-141361/15.

DR N-PSDB; AAF26897.

XX PT Screening the effect of an anti-gray hair agent.

XX PS Disclosure; Page 7-8; 11pp; Japanese.

XX CC The present invention describes a method for separating the mRNA encoding tyrosinase in a hair follicle for the assumption of hair colour and for screening an anti-gray hair agent. The method is useful for screening an anti-gray hair agent and judging the effect of it. The present sequence represents human tyrosinase which is given in the exemplification of the present invention

XX SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 4; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
 |||||  
 Db 448 DYSYLQSDPDPSFQD 462

RESULT 30

AAB86039

ID AAB86039 standard; protein; 529 AA.

XX AC AAB86039;

XX XX 16-JUL-2001 (first entry)

XX DE Human tyrosinase protein.

XX KW Listeria; expression vector; tumor-associated antigen; Trp 1; Trp 2;

KW MelanA/MART-1; cytostatic; attenuated; immunotherapy; malignant melanoma;  
 KW pigmented tumor; malignant schwannoma; vaccination; tyrosinase;  
 KW antigen-presenting cell.

XX OS Homo sapiens.

XX XX WO200127295-A1.

XX PD 19-APR-2001.

XX PF 13-OCT-2000; 2000WO-DE003629.

XX PR 14-OCT-1999; 99DE-01049594.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Schadendorf D, Paschen A, Chakraborty T, Domann E;

XX DR WPI; 2001-282041/29.

XX DR N-PSDB; AAF88041.

XX PT Listeria expression vector for immunotherapy, particularly of malignant melanoma, comprises a DNA sequence encoding tumor-associated antigens.

XX PS Disclosure; Fig 1; 41pp; German.

XX CC This invention describes a novel Listeria expression vector (A) for immunotherapy which comprises a promoter (P), functional in Listeria, operably linked to a DNA sequence (I) encoding one of the tumor-associated antigens (II) human tyrosinase, Trp 1 or 2, or MelanA/MART-1. The products of the invention have cytostatic activity. Recombinant attenuated Listeria containing (A) are useful for immunotherapy (prophylactic, adjuvant or therapeutic), specifically of malignant melanoma (but also other pigmented tumors such as malignant schwannoma), particularly as a replacement for radiotherapy. Using attenuated Listeria as carrier for (A) provides a simple way of vaccination, since antigen-presenting cells acquire tumor-associated antigens by natural infection, eliminating the need for labor-intensive ex vivo modification of autologous cells. This sequence represents the human tyrosinase protein described in the method of the invention

XX SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 4; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
 |||||  
 Db 448 DYSYLQSDPDPSFQD 462

RESULT 31

AAU84806

ID AAU84806 standard; protein; 529 AA.

XX AC AAU84806;

XX DT 08-MAY-2002 (first entry)

XX DE Human Tyros consensus sequence.

XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
 KW viral infection; human immunodeficiency virus; melanoma;  
 KW bacterial infection; Salmonella; Legionella; parasitic infection;  
 KW Trypanosoma; Toxoplasma; Giardia.

XX OS Homo sapiens.

XX XX WO200190197-A1.

XX PD 29-NOV-2001.

PF 25-MAY-2001; 2001WO-AU000622.  
 XX  
 PR 26-MAY-2000; 2000AU-00007761.  
 XX  
 PA (AUSU ) UNIV AUSTRALIAN NAT.  
 XX  
 PA Thomson SA, Ramshaw IA;  
 FI  
 XX WPI; 2002-147575/19.  
 DR  
 XX

PT New synthetic polypeptides having several different segments of at least  
 PT one parent polypeptide linked together differently compared to the  
 PT linkage in the parent polypeptide, for inducing immune response against a  
 PT pathogen or cancer.  
 XX

PS Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising  
 CC several different segments of at least one parent polypeptide linked  
 CC together in a different relationship relative to their linkage in the  
 CC parent polypeptide to impede, abrogate or otherwise alter at least one  
 CC function associated with the parent polypeptide and for inducing an  
 CC immune response against a pathogen or cancer. Also included are a  
 CC synthetic polynucleotide encoding and a computer system for designing the  
 CC synthetic polypeptides. The synthetic polypeptides and polynucleotides  
 CC are referred to as a Savine. The synthetic polypeptide is useful for  
 CC modulating immune responses preferably directed against a pathogen or a  
 CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head  
 CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,  
 CC oesophagus, brain, testicle, uterus), as potentiating agents.  
 CC Compositions comprising the polypeptide may be used in the treatment or  
 CC prophylaxis against viral (such as infections caused by HIV (human  
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic  
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is  
 CC a consensus sequence for a parent protein used to design a savine of the  
 CC invention  
 XX

SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 5; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15  
 |||||  
 Db 448 DYSYLQSDPDPSFQD 462

RESULT 32  
 AAU11544  
 ID AAU11544 standard; protein; 529 AA.  
 XX  
 AC AAU11544;

XX 12-MAR-2002 (first entry)  
 DT  
 XX Human Melanoma tumour associated antigen tyrosinase.  
 DE  
 XX

XX Human; melanoma tumour associated antigen; human leukocyte antigen;  
 KW major histocompatibility complex; MHC; HLA-A2.2; vaccine; cancer; HIV;  
 KW human immunodeficiency virus infection; cytostatic; virucide;  
 KW housekeeping epitope; adoptive immunotherapy; neoplastic disease;  
 KW viral disease; hepatitis virus; papilloma virus; tumour; leukaemia;  
 KW lymphoma; breast cancer; prostate cancer; lung cancer; tyrosinase;  
 KW parasitic infection; Chlamydia; Trypanosoma; Toxoplasma.

OS Homo sapiens.

XX WO200182963-A2.

FN

XX 08-NOV-2001.

XX 27-APR-2001; 2001WO-US013806.

XX 28-APR-2000; 2000US-00560465.

PR 28-APR-2000; 2000US-00561074.

PR 28-APR-2000; 2000US-00561571.

PR 28-APR-2000; 2000US-00561572.

XX (CTLI-) CTL IMMUNOTHERAPIES CORP.

XX Simard JUL, Diamond DC, Lei X;

XX WPI; 2002-066492/09.

PT Novel vaccine useful for treating neoplastic and viral diseases,  
 PT comprises a first housekeeping epitope derived from a first antigen  
 PT associated with a first target cell.

XX Example 24; Fig 18; 131pp; English.

XX The invention relates to a vaccine comprising a first housekeeping  
 CC epitope derived from a first antigen associated with a first target cell.  
 CC Also included are an isolated T cell expressing a T cell receptor  
 CC specific for a major histocompatibility complex (MHC)-peptide complex  
 CC comprising a first housekeeping epitope which is derived from a first  
 CC antigen associated with a first target cell, selecting an epitope (or  
 CC peptide sequence) from a population of peptide fragments of an antigen  
 CC associated with a target in a host, where the fragments have a known or  
 CC predicted affinity for a MHC receptor peptide binding cleft of the host,  
 CC where the epitope selected corresponds to a product of proteolytic  
 CC cleavage of the antigen in a cell of the host and a nucleic acid  
 CC construct comprising a first coding region, where the first coding region  
 CC comprises a first sequence encoding at least a first polypeptide, where  
 CC the first polypeptide comprises a first housekeeping epitope derived from  
 CC a first antigen associated with a first target cell; The epitopes,  
 CC peptides, vaccines and nucleic acids are useful in the manufacture of a  
 CC medicament for use in adoptive immunotherapy and for prevention and  
 CC treatment of neoplastic and viral diseases (e.g. human immunodeficiency  
 CC virus, HIV, infection, hepatitis virus and papilloma virus), cancers  
 CC (e.g. tumours, leukaemia, lymphoma, breast cancer, prostate cancer and  
 CC lung cancer), infection of cells by intracellular parasites (e.g.  
 CC Chlamydia, Trypanosoma and Toxoplasma) and many other examples given in  
 CC the specification. The invention permits the vaccine designer to ignore  
 CC peptides that, despite predicted high binding affinity for MHC, will  
 CC never be useful because they cannot be presented by target cells. The  
 CC invention provides a major advance in vaccine design, one that combines  
 CC the power of antigen sequence analysis with the fundamental realities of  
 CC immunology. The invention allows for the simple and effective selection  
 CC of meaningful epitopes for creation of MHC Class I or Class II vaccines  
 CC using any polypeptide sequence corresponding to a desired target. The  
 CC present sequence is an HLA-A2.1 (human leukocyte antigen) presenting  
 CC target cell protein from which epitopes of the invention may be derived,  
 CC tyrosinase (a melanoma tumour associated antigen)

XX SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 5; Length 529;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15

|||||  
 Db 448 DYSYLQSDPDPSFQD 462

RESULT 33

ABP74129

ID ABP74129 standard; protein; 529 AA.

XX AC ABP74129;

XX

DT 03-FEB-2003 (first entry)  
XX Human tyrosinase protein SEQ ID NO:2.  
DE Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;  
XX T cell; enzyme.  
KW Homo sapiens.  
XX WO200281646-A2.  
XX 17-OCT-2002.  
XX 04-APR-2002; 2002WO-US011101.  
XX 06-APR-2001; 2001US-0282211P.  
PR 07-NOV-2001; 2001US-0337017P.  
PR 07-MAR-2002; 2002US-0363210P.  
XX (CTLI-) CTL IMMUNOTHERAPIES CORP.  
XX Simard JUL, Diamond DC, Liu L, Xie Z;  
XX WPI; 2003-067518/06.  
DR N-PSDB; ABQ83843.  
XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid  
PT encoding the peptides, that are useful epitopes of target-associated  
PT antigens.  
XX Claim 1; Page 145; 352pp; English.  
XX The present invention describes an isolated epitope (I) and an epitope  
CC cluster. Also described is a vaccine or immunotherapeutic composition  
CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for  
CC treating an animal, by administering to an animal the vaccine or  
CC immunotherapeutic composition. VC is also useful for evaluating  
CC immunogenicity of a vaccine or immunotherapeutic composition, by  
CC administering VC to an HLA-transgenic animal and evaluating  
CC immunogenicity based on a characteristic of the animal, or by in vitro  
CC primary stimulation of a T cell and evaluating immunogenicity. (I) is  
CC useful for determining specific T cell frequency, by contacting T cells  
CC with a MHC-peptide complex, and further comprises ELISPOT analysis,  
CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or  
CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to  
CC ABP74713 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 529 AA;  
Query Match 100.0%; Score 83; DB 6; Length 529;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05; Mismatches 0; Indels 0; Gaps 0;  
Matches 15; Conservative 0;  
QY 1 DYSYLQSDPDSPQD 15  
|||  
Db 448 DYSYLQSDPDSPQD 462  
RESULT 34  
ABR83439  
ID ABR83439 standard; protein; 529 AA.  
XX ABR83439;  
XX 13-OCT-2003 (first entry)  
XX Human tyrosinase amino acid sequence SEQ ID NO:4.  
XX Epitope cluster; cytostatic; virucide; antibacterial; protozoacide;  
KW fungicide; vaccine; adoptive immunotherapy; immune response; cancer;  
KW intracellular parasite; infection; immunotherapeutic; neoplastic disease;  
KW viral disease; human; carcinoembryonic antigen; CEA.

XX Homo sapiens.  
XX WO2003057823-A2.  
XX 17-JUL-2003.  
XX 05-NOV-2002; 2002WO-US035582.  
XX 07-NOV-2001; 2001US-00005905.  
PR 07-DEC-2001; 2001US-00026066.  
XX (CTLI-) CTL IMMUNOTHERAPIES CORP.  
XX Simard JUL, Diamond DC;  
XX WPI; 2003-577518/54.  
XX New epitope cluster derived from an antigen associated with a target,  
PT useful for treating or preventing neoplastic or viral diseases, or  
PT inducing an immune response against cancer cells or cells infected with  
PT intracellular parasites.  
XX Example 24; Fig 18; 190pp; English.  
XX The present invention describes an epitope cluster (I) derived from an  
CC antigen associated with a target, where the cluster is a fragment of the  
CC antigen. The cluster comprises or encodes at least two sequences having a  
CC known or predicted affinity for a major histocompatibility complex  
CC receptor-binding cleft. (I) has the structure: X-P21-XAN-P2N-X(bN-1)-P1-  
CC XAN-PN, where X = any amino acid naturally occurring in a protein  
CC sequence; Xa and X(b/-1) = strings of amino acids of length a and b/-1,  
CC respectively; a = the number of amino acids between P21 and P2N; (b-1) =  
CC the number of amino acids between P2N and P1; P21 = a first primary  
CC anchor and second residue of a first epitope; P2N = a first primary  
CC anchor and second residue of an Nth epitope; P1 = a last primary anchor  
CC and C-terminal residue of the first epitope; ZN, NC, N = the Nth epitope  
CC of the cluster; Nc = the total number of epitopes in the cluster; and aN  
CC and bN = the positional relationship between the first and Nth epitope.  
CC (I) has cytostatic, virucide, antibacterial, protozoacide and fungicide,  
CC and can be used in vaccines. T cells from the present invention can be  
CC used for manufacturing a medicament for adoptive immunotherapy. The  
CC epitope clusters, polypeptides, polynucleotides or vaccines from the  
CC present invention can be used for inducing an immune response against  
CC cancer cells or cells infected with intracellular parasites such as  
CC viruses, bacteria, protozoa, fungi or prion. The T cell or  
CC immunotherapeutic composition from the present invention can be used for  
CC treating or preventing neoplastic or viral diseases. The present sequence  
CC is used in the exemplification of the present invention  
XX  
SQ Sequence 529 AA;  
Query Match 100.0%; Score 83; DB 6; Length 529;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05; Mismatches 0; Indels 0; Gaps 0;  
Matches 15; Conservative 0;  
QY 1 DYSYLQSDPDSPQD 15  
|||  
Db 448 DYSYLQSDPDSPQD 462  
RESULT 35  
ADC09566  
ID ADC09566 standard; protein; 529 AA.  
XX ADC09566;  
XX 18-DEC-2003 (first entry)  
XX Tyrosinase protein #SEQ ID 2.  
XX Epitope; immunological; vaccine;  
KW major histocompatibility complex class I; MHC class I; cancer;

immunisation.  
 Unidentified.  
 WO2003008537-A2.  
 30-JAN-2003.  
 29-MAR-2002; 2002WO-US010189.  
 06-APR-2001; 2001US-0282211P.  
 07-NOV-2001; 2001US-0337017P.  
 07-MAR-2002; 2002US-0363210P.  
 (CTLI-) CTL IMMUNOTHERAPIES CORP.  
 Simard JUL, Diamond DC, Liu L, Xie Z;  
 WPI; 2003-248010/24.  
 Epitope having high affinity for major histocompatibility complex class I useful for treating an animal, evaluating immunogenicity of a vaccine or therapeutic composition and for diagnosing a disease.  
 Claim 1; SEQ ID NO 2; 239pp; English.  
 The invention relates to an isolated epitope polypeptide that has high affinity for major histocompatibility complex (MHC) class I, and an epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, chemotherapy, biochemotherapy or surgery. The composition is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC-peptide complexes of the invention are useful for determining specific T cell frequency. This method is useful for evaluating immunological response, by performing the method prior to and subsequent to an immunisation step. Compositions of the invention are useful for diagnosing a disease. The current sequence represents an epitope of the invention with high affinity for MHC class I.  
 Sequence 529 AA;  
 Query Match 100.0%; Score 83; DB 7; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDPSFQD 15  
 |||||  
 Db 448 DYSYLQSDPDPSFQD 462  
 RESULT 36  
 AAR07071  
 ID AAR07071 standard; protein; 531 AA.  
 XX  
 AC AAR07071;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 09-MAR-1992 (first entry)  
 XX  
 DE Sequence encoded by human tyrosinase BBTY-1 cDNA.  
 XX  
 KW Tyrosinase; enzyme; melanosomes; melanin; melanocyte.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= signal  
 FT Protein 20..531  
 XX  
 FN WO9012869-A.

XX 01-NOV-1990.  
 XX PD  
 XX OS  
 XX PN 26-APR-1989; 89US-00343960.  
 XX PF  
 XX PR 26-APR-1989; 89US-00343960.  
 XX PR  
 XX PA (SLOK) SLOAN KETTERING INST CANCER.  
 XX PI  
 XX PI Bouchard B, Houghton A;  
 XX WPI; 1990-348472/46.  
 DR N-PSDB; AAQ06552.  
 XX  
 XX Non-melanocyte eukaryotic cell - expressing biologically active human tyrosinase and used in studying tyrosine synthesis.  
 XX PT  
 XX PS Disclosure; Fig 1; 49pp; English.  
 XX CC  
 CC A cDNA library was constructed from mRNA prepared from the human melanotic melanoma cell line SK-MEL-19. For screening, a 50 base probe was used (see AAQ06551). The cDNA clone BBTY-1 was isolated, sequenced (see AAQ06552) and analysed for tyrosinase activity. (Updated on 25-MAR-2003 to correct PA field.)  
 XX CC  
 XX SQ Sequence 531 AA;  
 Query Match 100.0%; Score 83; DB 2; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDPSFQD 15  
 |||||  
 Db 450 DYSYLQSDPDPSFQD 464  
 RESULT 37  
 AAR79493  
 ID AAR79493 standard; protein; 531 AA.  
 XX  
 AC AAR79493;  
 XX  
 DT 10-FEB-1996 (first entry)  
 XX  
 DE Human tyrosinase acting as a tumor rejection antigen precursor.  
 XX  
 KW Tumor rejection antigen precursor; tyrosinase; enzyme; tumor therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9523234-A1.  
 XX  
 PD 31-AUG-1995.  
 XX  
 PF 16-FEB-1995; 95WO-US001990.  
 XX  
 PR 28-FEB-1994; 94US-00203054.  
 PR 26-APR-1994; 94US-00233305.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Wolfel T, Van Pel A, Brichard V, Boon-Falleur T;  
 XX WPI; 1995-311542/40.  
 DR N-PSDB; AAT01009.  
 XX  
 XX Cytolytic T cell specific for MHC complexes - used to treat individual(s) with cellular abnormality, e.g. tumour(s).  
 FT  
 XX Disclosure; Page 30-33; 57pp; English.  
 XX  
 CC Human tyrosinase may act as a tumor rejection antigen precursor (TRAP) and be processed to form a peptide tumor rejection antigen which is

CC presented on the surface of the cell, in combination with HLA-A2, thereby  
 CC stimulating lysis by cytotoxic T-lymphocyte clones  
 XX  
 SQ Sequence 531 AA;  
 Query Match 100.0%; Score 83; DB 2; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDSPFQD 15  
 Db 450 DYSYLQSDPDSPFQD 464  
 RESULT 38  
 AAW22083  
 ID AAW22083 standard; protein; 531 AA.  
 XX  
 AC AAW22083;  
 DT 24-DEC-1997 (first entry)  
 XX Human SK29-MEL tyrosinase.  
 DE Tyrosine; tumour rejection antigen; TRAP; human leukocyte antigen;  
 KW HLA-B44; SK29-MEL; major histocompatibility complex; MHC;  
 KW cellular abnormality; melanoma; autoimmune disease; gene therapy;  
 KW diagnosis.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..17  
 FT Protein 18..531  
 FT Misc-difference 34 /label= Mat\_protein  
 FT /note= "encoded by GAG"  
 FT Misc-difference 181  
 FT /note= "encoded by ATG"  
 FT Misc-difference 194  
 FT /note= "encoded by TCT"  
 FT Misc-difference 223  
 FT /note= "encoded by GAA"  
 FT Misc-difference 231  
 FT /note= "encoded by GAA"  
 FT Misc-difference 252  
 FT /note= "encoded by GAG"  
 FT Misc-difference 404  
 FT /note= "encoded by CAA"  
 FT Misc-difference 471  
 FT /note= "encoded by GAA"  
 XX WO9726535-A1.  
 XX  
 XX  
 PD 24-JUL-1997.  
 XX  
 XX 14-JAN-1997; 97WO-US000834.  
 XX  
 XX 17-JAN-1996; 96US-00587391.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 XX Lethe B, Brichard V, Van Pel A, Boon-Falleur T, Wolfel T;  
 PI  
 XX WPI; 1997-385477/35.  
 DR N-PSDB; AAT75678.  
 XX  
 XX Complex of human leukocyte antigen and tyrosinase peptide - used for  
 PT treating cellular abnormalities, e.g. tumours.  
 XX  
 PS Example 5; Page 34-37; 64pp; English.  
 CC

CC This polypeptide comprises a human tyrosinase whose sequence was deduced  
 CC from a cDNA clone (see AAT75678) which was isolated from cell line  
 CC melanoma SK29-MEL.1 following a screen for clones that stimulated  
 CC cytolytic T cell lines CTL 210/9 and CTL IVSB. Human tyrosinase acts as a  
 CC tumour rejection antigen precursor and is processed to form a peptide  
 CC tumour rejection antigen (see AAW22082) that is presented on the surface  
 CC of a cell in combination with HLA-A2, thereby stimulating lysis by CTL  
 CC clones. Methods are claimed for identifying individuals having abnormal  
 CC cells that present complexes of the tumour rejection antigen and HLA-B44,  
 CC for treating such individuals (e.g. by administering vectors that code  
 CC for human tyrosinase and an HLA-B44 molecule), for isolating cytolytic T  
 CC cells specific for the complex of HLA-B44 and the peptide, and for  
 CC identifying abnormal cells. The methods can be used to treat tumours,  
 CC such as melanoma, autoimmune disorders, etc  
 XX  
 SQ Sequence 531 AA;  
 Query Match 100.0%; Score 83; DB 2; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDSPFQD 15  
 Db 450 DYSYLQSDPDSPFQD 464  
 RESULT 39  
 AAW38165  
 ID AAW38165 standard; protein; 560 AA.  
 XX  
 AC AAW38165;  
 DT 13-MAR-1998 (first entry)  
 XX Human tyrosinase.  
 DE  
 KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;  
 KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;  
 KW tyrosinase.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..12  
 FT /label= sig\_peptide  
 FT Peptide 13..560  
 FT /label= mat\_peptide  
 XX US5679511-A.  
 XX  
 XX 21-OCT-1997.  
 XX  
 XX 01-JUN-1992; 92US-00891942.  
 XX  
 XX 06-OCT-1986; 86US-00915753.  
 PR 07-JUN-1989; 89US-00362847.  
 XX  
 XX (GUTH-) GUTHRIE FOUND MEDICAL RES INC DONALD.  
 PA (INDV ) UNIV INDIANA FOUND.  
 XX  
 XX Kwon BS;  
 XX  
 XX WPI; 1997-525715/48.  
 DR N-PSDB; AAT95732.  
 XX  
 XX Lambda mel 17-1 cDNA and Pmel17 protein - useful as melanin biosynthesis  
 FT probe.  
 XX  
 XX Disclosure; Col 47-52; 67pp; English.  
 XX  
 CC The present sequence is disclosed in the specification, which describes  
 CC the isolation of Pmel17, a protein encoded by cDNA isolated from lambda  
 CC mel 17-1 (ATCC 40264). The degree of melanisation in a human melanocyte

CC can be determined by subjecting human melanocyte RNA to a Northern blot  
CC analysis, using the cDNA as a probe

SQ Sequence 560 AA;

Query Match 100.0%; Score 83; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 9.9e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15

Db 446 DYSYLQSDPDPSFQD 460

RESULT 40

AAU85008  
ID AAU85008 standard; protein; 5546 AA.

XX AC AAU85008;

XX DT 08-MAY-2002 (first entry)

XX DE Human melanocyte differentiation antigens savine.

XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
KW viral infection; human immunodeficiency virus; melanoma;  
KW bacterial infection; Salmonella; Legionella; parasitic infection;  
KW Trypanosoma; Toxoplasma; Giardia.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200190197-A1.

XX PD 29-NOV-2001.

XX PF 25-MAY-2001; 2001WO-AU000622.

XX PR 26-MAY-2000; 2000AU-00007761.

XX PA (AUSU ) UNIV AUSTRALIAN NAT.

XX PI Thomson SA, Ramshaw IA;

XX DR WPI; 2002-147575/19.

XX DR N-PSDB; ABK36828.

XX PT New synthetic polypeptides having several different segments of at least  
PT one parent polypeptide linked together differently compared to the  
PT linkage in the parent polypeptide, for inducing immune response against a  
PT pathogen or cancer.

XX PS Example 3; Fig 27; 364pp; English.

XX CC The invention relates to a new synthetic polypeptide (I) comprising  
CC several different segments of at least one parent polypeptide linked  
CC together in a different relationship relative to their linkage in the  
CC parent polypeptide to impede, abrogate or otherwise alter at least one  
CC function associated with the parent polypeptide and for inducing an  
CC immune response against a pathogen or cancer. Also included are a  
CC synthetic polynucleotide encoding and a computer system for designing the  
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides  
CC are referred to as a Savine. The synthetic polypeptide is useful for  
CC modulating immune responses preferably directed against a pathogen or a  
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head  
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,  
CC oesophagus, brain, testicle, uterus), as potentiating agents.  
CC Compositions comprising the polypeptide may be used in the treatment or  
CC prophylaxis against viral (such as infections caused by HIV (human  
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic

CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is  
CC a savine protein of the invention

SQ Sequence 5546 AA;

Query Match 100.0%; Score 83; DB 5; Length 5546;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15

Db 75 DYSYLQSDPDPSFQD 89

Search completed: June 3, 2004, 17:10:09

Job time : 57 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:14:49 ; Search time 39 seconds  
(without alignments)  
108.207 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DYSYLQSDSPDSFQD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

# Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	15	9	US-09-923-831-26
2	83	100.0	15	9	US-09-766-889A-38
3	83	100.0	15	12	US-10-218-095-33
4	83	100.0	15	14	US-10-161-097-25
5	83	100.0	15	14	US-10-170-832-67
6	83	100.0	30	12	US-10-296-734-1030
7	83	100.0	43	16	US-10-447-161-142
8	83	100.0	529	12	US-10-296-734-820
9	83	100.0	529	12	US-10-253-286-487
10	83	100.0	529	13	US-10-011-436-4
11	83	100.0	529	15	US-10-026-066-4
12	83	100.0	529	15	US-10-117-937-2
13	83	100.0	529	15	US-10-245-871-487
14	83	100.0	546	12	US-10-296-734-1210
15	77	92.8	30	12	US-10-296-734-1032

16	70	84.3	13	9	US-09-847-185-42	Sequence 42, Appl
17	70	84.3	13	14	US-10-224-286-42	Sequence 42, Appl
18	70	84.3	13	15	US-10-406-317-14	Sequence 14, Appl
19	70	84.3	13	16	US-10-676-909-30	Sequence 30, Appl
20	70	84.3	13	16	US-10-297-168-14	Sequence 14, Appl
21	54	65.1	533	14	US-10-207-655-75	Sequence 75, Appl
22	49	59.0	394	15	US-10-231-913-42	Sequence 42, Appl
23	48	57.8	695	10	US-09-374-046A-132	Sequence 132, App
24	48	57.8	695	12	US-10-616-263-132	Sequence 91, Appl
25	48	57.8	696	9	US-09-909-320-91	Sequence 91, Appl
26	48	57.8	696	9	US-09-909-088B-91	Sequence 91, Appl
27	48	57.8	696	9	US-09-905-291A-91	Sequence 91, Appl
28	48	57.8	696	9	US-09-902-853-91	Sequence 91, Appl
29	48	57.8	696	9	US-09-907-824-91	Sequence 91, Appl
30	48	57.8	696	9	US-09-907-841-91	Sequence 91, Appl
31	48	57.8	696	10	US-09-904-011-91	Sequence 91, Appl
32	48	57.8	696	10	US-09-906-742-91	Sequence 91, Appl
33	48	57.8	696	10	US-09-906-838-91	Sequence 91, Appl
34	48	57.8	696	10	US-09-907-613-91	Sequence 91, Appl
35	48	57.8	696	10	US-09-907-942-91	Sequence 91, Appl
36	48	57.8	696	10	US-09-904-859-91	Sequence 91, Appl
37	48	57.8	696	10	US-09-909-204-91	Sequence 91, Appl
38	48	57.8	696	10	US-09-904-820-91	Sequence 91, Appl
39	48	57.8	696	10	US-09-904-786-91	Sequence 91, Appl
40	48	57.8	696	10	US-09-906-646-91	Sequence 91, Appl
41	48	57.8	696	10	US-09-906-700-91	Sequence 91, Appl
42	48	57.8	696	10	US-09-903-786-91	Sequence 91, Appl
43	48	57.8	696	10	US-09-902-903-91	Sequence 91, Appl
44	48	57.8	696	10	US-09-903-749A-91	Sequence 91, Appl
45	48	57.8	696	10	US-09-904-119-91	Sequence 91, Appl

## ALIGNMENTS

RESULT 1  
US-09-923-831-26  
; Sequence 26, Application US/09923831  
; Patent No. US20020115142A1  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val,rie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/923,831  
; PRIOR FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 09/183,706  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 26  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-831-26

Query Match 100.0% Score 83; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDSPDSFQD 15  
Db 1 DYSYLQSDSPDSFQD 15

RESULT 2  
US-09-766-889A-38  
; Sequence 38, Application US/09766889A  
; Patent No. US20020164654A1  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre

; APPLICANT: Stroobant, Vincent  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: Schultze, Erwin  
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
; CURRENT APPLICATION NUMBER: US/09/766,889A  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US 60/177,242  
; PRIOR FILING DATE: 2000-01-20  
; PRIOR APPLICATION NUMBER: US 60/243,212  
; PRIOR FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 38  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-766-889A-38

Query Match 100.0%; Score 83; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
|||  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 3  
US-10-218-095-33  
; Sequence 33, Application US/10218095  
; Publication No. US20040033541A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Yi  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Russo, Vincenzo  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF  
; FILE REFERENCE: L00461/70137  
; CURRENT APPLICATION NUMBER: US/10/218,095  
; CURRENT FILING DATE: 2002-08-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-218-095-33

Query Match 100.0%; Score 83; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
|||  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 4  
US-10-161-097-25  
; Sequence 25, Application US/10161097  
; Publication No. US20030096404A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENZWEIG, Michael  
; APPLICANT: PYKETT, Mark J.  
; APPLICANT: SCADDEN, David T.  
; APPLICANT: POZNANSKY, Mark C.  
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
; TITLE OF INVENTION: DEVICES  
; FILE REFERENCE: C1005/7012/KA/ERG  
; CURRENT APPLICATION NUMBER: US/10/161,097

; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US/09/574,749  
; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/107,972  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: PCT/US99/26795  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/524,749  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Homo Sapiens source  
US-10-161-097-25

Query Match 100.0%; Score 83; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
|||  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 5  
US-10-170-832-67  
; Sequence 67, Application US/10170832  
; Publication No. US20030170792A1  
; GENERAL INFORMATION:  
; APPLICANT: Chau, Pascal  
; APPLICANT: Vantomme, Valrie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Corthals, Jorgen  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/10/170,832  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US/09/166,448  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-832-67

Query Match 100.0%; Score 83; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
|||  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 6  
US-10-296-734-1030  
; Sequence 1030, Application US/10296734  
; Publication No. US20040054137A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Scott A  
; APPLICANT: Ranehaw, Ian A  
; TITLE OF INVENTION: Synthetic molecules and uses therefor  
; FILE REFERENCE: Savine  
; CURRENT APPLICATION NUMBER: US/10/296,734

; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: AU PQ7761/00  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 1507  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1030  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: tyros segment 30  
US-10-296-734-1030

Query Match 100.0%; Score 83; DB 12; Length 30;  
Best Local Similarity 100.0%; Pred. No. 7.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
DB 15 DYSYLQSDPDPSFQD 29

## RESULT 7

US-10-447-161-142  
; Sequence 142, Application US/10447161  
; Publication No. US20040023314A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Rong-fu  
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis  
; FILE REFERENCE: HO-P02484U1  
; CURRENT APPLICATION NUMBER: US/10/447,161  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: 60/383,530  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 142  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-447-161-142

Query Match 100.0%; Score 83; DB 16; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
DB 16 DYSYLQSDPDPSFQD 30

## RESULT 8

US-10-296-734-820  
; Sequence 820, Application US/10296734  
; Publication No. US20040054137A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Scott A  
; APPLICANT: Ramshaw, Ian A  
; TITLE OF INVENTION: Synthetic molecules and uses therefor  
; FILE REFERENCE: Savine  
; CURRENT APPLICATION NUMBER: US/10/296,734  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: AU PQ7761/00  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 1507  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 820  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:

; OTHER INFORMATION: Tyros consensus polypeptide  
US-10-296-734-820

Query Match 100.0%; Score 83; DB 12; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
DB 448 DYSYLQSDPDPSFQD 462

## RESULT 9

US-10-253-286-487  
; Sequence 487, Application US/10253286  
; Publication No. US20040058881A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2015  
; CURRENT APPLICATION NUMBER: US/10/253,286  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 487  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-253-286-487

Query Match 100.0%; Score 83; DB 12; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
DB 448 DYSYLQSDPDPSFQD 462

## RESULT 10

US-10-011-436-4  
; Sequence 4, Application US/10011436  
; Publication No. US20020128200A1  
; GENERAL INFORMATION:  
; APPLICANT: Boon-Falleur, Thierry; Brichard, Vincent; Van Pel,  
; Aline;  
; Deplaen, Etienne; Coulie, Pierre; Renaud, Jean Christophe; Wolfel,  
; Lethe, Bernard  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING INDIVIDUALS SUFFERING FROM  
; A  
; CELLULAR ABNORMALITY SOME OF WHOSE ABNORMAL CELLS PRESENT C  
; LEUKOCYTE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 801 Pennsylvania Avenue N.W.  
; CITY: Washington  
; STATE: District of Columbia  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.25inch, 1.44MB storage  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/011,436  
; FILING DATE: 11-Dec-2001

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/511,011  
FILING DATE: 5-AUGUST-1995  
APPLICATION NUMBER: 08/054,714  
FILING DATE: 28-APRIL-1993  
APPLICATION NUMBER: 07/994,928  
FILING DATE: 22-DECEMBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mary Anne Schofield  
REGISTRATION NUMBER: 36,669  
REFERENCE/DOCKET NUMBER: LUD 5299.9 DIV CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 662-0200  
TELEFAX: (202) 662-4643  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 529  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-011-436-4

Query Match 100.0%; Score 83; DB 13; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
|||||  
DB 448 DYSYLQSDPDPSFQD 462

RESULT 11  
US-10-026-066-4  
Sequence 4, Application US/10026066  
Publication No. US20030215425A1  
GENERAL INFORMATION:  
APPLICANT: Simard, John J. L.  
APPLICANT: Diamond, David C.  
TITLE OF INVENTION: EPIOTOPE SYNCHRONIZATION IN ANTIGEN  
TITLE OF INVENTION: PRESENTING CELLS  
FILE REFERENCE: CTLLM-21C1C  
CURRENT APPLICATION NUMBER: US/10/026,066  
CURRENT FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: 09/561,074  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 09/560,465  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 09/561,572  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 09/561,571  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: PCT/US01/13806  
PRIOR FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 529  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-026-066-4

Query Match 100.0%; Score 83; DB 15; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
|||||  
DB 448 DYSYLQSDPDPSFQD 462

RESULT 12

US-10-117-937-2  
Sequence 2, Application US/10117937  
Publication No. US20030220239A1  
GENERAL INFORMATION:  
APPLICANT: CTL IMMUNO THERAPIES CORP.  
APPLICANT: SIMARD, John, J.L.  
APPLICANT: DIAMOND, David, C.  
APPLICANT: LIU, Liping  
APPLICANT: XIE, Zhidong  
TITLE OF INVENTION: EPIOTOPE SEQUENCES  
FILE REFERENCE: CTLLM-027A  
CURRENT APPLICATION NUMBER: US/10/117,937  
CURRENT FILING DATE: 2002-04-04  
PRIOR APPLICATION NUMBER: US 60/282,211  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: US 60/337,017  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/363,210  
PRIOR FILING DATE: 2002-03-07  
NUMBER OF SEQ ID NOS: 602  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 529  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-117-937-2

Query Match 100.0%; Score 83; DB 15; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
|||||  
DB 448 DYSYLQSDPDPSFQD 462

RESULT 13  
US-10-245-871-487  
Sequence 487, Application US/10245871  
Publication No. US20030235594A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2013  
CURRENT APPLICATION NUMBER: US/10/245,871  
CURRENT FILING DATE: 2003-01-09  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 905  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 487  
LENGTH: 529  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-245-871-487

Query Match 100.0%; Score 83; DB 15; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
|||||  
DB 448 DYSYLQSDPDPSFQD 462

RESULT 14  
US-10-296-734-1210  
Sequence 1210, Application US/10296734  
Publication No. US20040054137A1  
GENERAL INFORMATION:

; APPLICANT: Thompson, Scott A  
; APPLICANT: Ramshaw, Ian A  
; TITLE OF INVENTION: Synthetic molecules and uses therefor  
; FILE REFERENCE: Savine  
; CURRENT APPLICATION NUMBER: US/10/296,734  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: AU PQ7761/00  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 1507  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1210  
; LENGTH: 5546  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Differentiation svaine  
US-10-296-734-1210

Query Match 100.0%; Score 83; DB 12; Length 5546;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSYLQSDSDPSFQD 15  
DB 75 DSYLQSDSDPSFQD 89

RESULT 15  
US-10-296-734-1032  
; Sequence 1032, Application US/10296734  
; Publication No. US20040054137A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Scott A  
; APPLICANT: Ramshaw, Ian A  
; TITLE OF INVENTION: Synthetic molecules and uses therefor  
; FILE REFERENCE: Savine  
; CURRENT APPLICATION NUMBER: US/10/236,734  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: AU PQ7761/00  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 1507  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1032  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: tyros segment 31  
US-10-296-734-1032

Query Match 92.8%; Score 77; DB 12; Length 30;  
Best Local Similarity 100.0%; Pred. No. 6.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSYLQSDSDPSFQD 15  
DB 1 YSYLQSDSDPSFQD 14

Search completed: June 3, 2004, 15:24:23  
Job time : 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 17:08:22 ; Search time 23 Seconds  
(without alignments)  
33.669 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DYSYLQSDPDSPDQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	15	2	US-09-036-582-23
2	83	100.0	15	3	US-09-183-706-26
3	83	100.0	15	3	US-09-166-448-67
4	83	100.0	15	4	US-09-567-995-26
5	83	100.0	15	4	US-09-165-863-23
6	83	100.0	15	4	US-09-697-884-67
7	83	100.0	15	4	US-09-289-350-23
8	83	100.0	15	4	US-09-574-749B-25
9	83	100.0	15	4	US-09-318-141-23
10	83	100.0	15	4	US-09-169-717E-29
11	83	100.0	508	1	US-07-891-942G-10
12	83	100.0	529	1	US-07-891-942G-10
13	83	100.0	529	2	US-08-370-909-19
14	83	100.0	529	2	US-08-504-048-8
15	83	100.0	529	4	US-09-341-982-1
16	83	100.0	529	4	US-09-169-717E-39
17	83	100.0	529	4	US-10-011-436-4
18	83	100.0	537	3	US-08-540-922D-12
19	83	100.0	560	1	US-07-891-942G-5
20	70	84.3	13	2	US-08-902-516-42
21	70	84.3	13	4	US-09-847-185-42
22	70	84.3	13	4	US-09-601-729-113
23	62	74.7	19	2	US-08-504-048-4
24	59	71.1	12	4	US-09-341-982-3
25	55	66.3	11	4	US-09-341-982-5
26	48	57.8	696	4	US-09-907-794A-91
27	48	57.8	696	4	US-09-905-125A-91

28	48	57.8	696	4	US-09-902-775A-91	Sequence 91, Appl
29	43	51.8	320	4	US-09-543-681A-4651	Sequence 4651, Ap
30	41	49.4	451	4	US-09-543-681A-4841	Sequence 4841, Ap
31	40	48.2	351	4	US-09-107-532A-4896	Sequence 4896, Ap
32	40	48.2	396	3	US-09-046-992-4	Sequence 4, Appli
33	40	48.2	420	1	US-08-391-259-2	Sequence 2, Appli
34	40	48.2	420	1	US-08-391-259-7	Sequence 7, Appli
35	40	48.2	420	1	US-08-391-259-10	Sequence 10, Appl
36	40	48.2	420	1	US-08-391-259-11	Sequence 11, Appl
37	40	48.2	420	2	US-08-839-425-2	Sequence 2, Appli
38	40	48.2	420	2	US-08-839-425-10	Sequence 10, Appl
39	40	48.2	420	2	US-08-839-425-11	Sequence 11, Appl
40	40	48.2	420	2	US-08-021-601-6	Sequence 6, Appli
41	40	48.2	456	1	US-08-082-849B-6	Sequence 6, Appli
42	40	48.2	456	5	PCT-US94-01624-6	Sequence 42, Appl
43	40	48.2	462	2	US-08-484-438-42	Sequence 8, Appli
44	40	48.2	472	1	US-08-021-601-8	
45	40	48.2				

## ALIGNMENTS

RESULT 1  
US-09-036-582-23  
; Sequence 23, Application US/09036582A  
; Patent No. 5965381  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Cornelis, Guy R.  
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
; TITLE OF INVENTION: WITH RECOMBINANT VERSINIA  
; FILE REFERENCE: 11154  
; CURRENT APPLICATION NUMBER: US/09/036,582A  
; CURRENT FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide  
; US-09-036-582-23

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDSPDQ 15 Asp Tyr Ser Tyr Leu Gln Asp Ser  
Db 1 DYSYLQSDPDSPDQ 15 Asp Pro Asp Ser Phe Gln Asp

RESULT 2  
US-09-183-706-26  
; Sequence 26, Application US/09183706  
; Patent No. 6245525  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Fallier, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/183,706  
; CURRENT FILING DATE: 1998-10-30  
; EARLIER APPLICATION NUMBER: 09/122,989  
; EARLIER FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 26  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-183-706-26

Query Match 100.0%; Score 83; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15  
Db 1 DYSYLQSDPDPSFQD 15

## RESULT 3

US-09-166-448-67 OK  
; Sequence 67, Application US/09166448  
; Patent No. 6291430  
; GENERAL INFORMATION:  
; APPLICANT: Pascal  
; APPLICANT: Vantomme, Valrie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Corthals, Jurgien  
; TITLE OF INVENTION: WAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/09/166,448  
; CURRENT FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-166-448-67

Query Match 100.0%; Score 83; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15  
Db 1 DYSYLQSDPDPSFQD 15

## RESULT 4

US-09-567-995-26 OK  
; Sequence 26, Application US/09567995  
; Patent No. 6303756  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/567,995  
; CURRENT FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: 09/183,706  
; PRIOR FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 26  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-567-995-26

Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15  
Db 1 DYSYLQSDPDPSFQD 15

## RESULT 5

US-09-289-350-23

; Sequence 23, Application US/09289350

US-09-165-863-23  
; Sequence 23, Application US/09165863  
; Patent No. 6407063  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Duffour, Marie-Therese  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Cornelis, Guy  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Lurquin, Christophe  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: Chauv, Pascal  
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
; TITLE OF INVENTION: PROCEDURE  
; FILE REFERENCE: 11727  
; CURRENT APPLICATION NUMBER: US/09/165,863  
; CURRENT FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide  
US-09-165-863-23

Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15  
Db 1 DYSYLQSDPDPSFQD 15

## RESULT 6

US-09-697-884-67 OK  
; Sequence 67, Application US/09697884  
; Patent No. 6426217  
; GENERAL INFORMATION:  
; APPLICANT: Chauv, Pascal  
; APPLICANT: Vantomme, Valrie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Corthals, Jurgien  
; TITLE OF INVENTION: WAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/09/697,884  
; CURRENT FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: 09/166,448  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-697-884-67

Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15  
Db 1 DYSYLQSDPDPSFQD 15

## RESULT 7

US-09-289-350-23  
; Sequence 23, Application US/09289350



OK

Patent No. 6531451  
GENERAL INFORMATION:  
APPLICANT: Chau, Pascal  
APPLICANT: Luitten, Rosalie  
APPLICANT: Demotte, Nathalie  
APPLICANT: Delfour, Marie-Therese  
APPLICANT: Lurquin, Christophe  
APPLICANT: Traversari, Catia  
APPLICANT: Stroobant, Vincent  
APPLICANT: Cornelis, Guy R.  
APPLICANT: Boon-Falleur, Thierry  
APPLICANT: Van Der Bruggen, Pierre  
TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
TITLE OF INVENTION: PROCEDURE  
FILE REFERENCE: 11727Z  
CURRENT APPLICATION NUMBER: US/09/289,350  
CURRENT FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: 09/165,863  
PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 23  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Human Tyrosinase peptide  
US-09-289-350-23

Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
DB 1 DYSYLQSDPDPSFQD 15

OK

RESULT 8  
US-09-574-749B-25  
Sequence 25, Application US/09574749B  
Patent No. 6548299  
GENERAL INFORMATION:  
APPLICANT: ROSENZWEIG, Michael  
APPLICANT: PIKETT, Mark J.  
APPLICANT: SCADDEN, David T.  
APPLICANT: POZNANSKY, Mark C.  
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
FILE REFERENCE: C1005/7012/KA/ERG  
CURRENT APPLICATION NUMBER: US/09/574,749B  
CURRENT FILING DATE: 2002-05-31  
PRIOR APPLICATION NUMBER: US 60/107,972  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: PCT/US99/26795  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 09/524,749  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 25  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Homo Sapiens source  
US-09-574-749B-25

Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
DB 1 DYSYLQSDPDPSFQD 15

OK

Db 1 DYSYLQSDPDPSFQD 15

RESULT 9  
US-09-318-141-23  
Sequence 23, Application US/09318141  
Patent No. 6602506  
GENERAL INFORMATION:  
APPLICANT: van der Bruggen, Pierre  
APPLICANT: Cornelis, Guy R.  
TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
TITLE OF INVENTION: WITH RECOMBINANT YERSINIA  
FILE REFERENCE: 11154  
CURRENT APPLICATION NUMBER: US/09/318,141  
CURRENT FILING DATE: 1999-05-25  
EARLIER APPLICATION NUMBER: US 09/036,582  
EARLIER FILING DATE: 1998-03-06  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Human Tyrosinase peptide  
US-09-318-141-23

Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
DB 1 DYSYLQSDPDPSFQD 15

OK

RESULT 10  
US-09-169-717E-29  
Sequence 29, Application US/09169717E  
Patent No. 6667037  
GENERAL INFORMATION:  
APPLICANT: Ooms, Annie  
APPLICANT: Degiovanni, Gerard  
APPLICANT: Morel, Sandra  
APPLICANT: Van den Eynde, Benoit  
APPLICANT: Boon-Falleur, Thierry  
TITLE OF INVENTION: Isolator Peptides Which Bind To HLA-B35 Molecules,  
TITLE OF INVENTION: Larger Peptides Which Contain These, Nucleic Acid  
TITLE OF INVENTION: Molecules Encoding Peptides, And Uses Thereof  
FILE REFERENCE: LUD5561  
CURRENT APPLICATION NUMBER: US/09/169,717E  
CURRENT FILING DATE: 1998-10-09  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 29  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
US-09-169-717E-29

Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
DB 1 DYSYLQSDPDPSFQD 15

RESULT 11  
US-07-891-942G-10  
Sequence 10, Application US/07891942G  
Patent No. 5679511  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung Se

;; TITLE OF INVENTION: CDNA CLONES FOR HUMAN TYROSINASE AND FOR  
;; TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY  
;; NUMBER OF SEQUENCES: 16  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Christopher A. Michaels, Barnard, Brown &  
;; ADDRESSEE: Michaels  
;; STREET: 306 East State Street; Suite 220  
;; CITY: Ithaca  
;; STATE: NY  
;; COUNTRY: USA  
;; ZIP: 14850  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/891,942G  
;; FILING DATE: 01-JUN-1992  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 06/915,753  
;; FILING DATE: 06-OCT-1986  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 508 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-07-891-942G-10

Query Match 100.0%; Score 83; DB 1; Length 508;  
Best Local Similarity 100.0%; Pred. No. 9.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15  
|||||  
Db 448 DYSYLQSDPDSPDQ 462

RESULT 12  
US-07-891-942G-8  
;; Sequence 8, Application US/07891942G  
;; Patent No. 5679511  
;; GENERAL INFORMATION:  
;; APPLICANT: Kwon, Byoung Se  
;; TITLE OF INVENTION: CDNA CLONES FOR HUMAN TYROSINASE AND FOR  
;; TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY  
;; NUMBER OF SEQUENCES: 16  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Christopher A. Michaels, Barnard, Brown &  
;; ADDRESSEE: Michaels  
;; STREET: 306 East State Street; Suite 220  
;; CITY: Ithaca  
;; STATE: NY  
;; COUNTRY: USA  
;; ZIP: 14850  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/07/891,942G  
;; FILING DATE: 01-JUN-1992  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 06/915,753  
;; FILING DATE: 06-OCT-1986  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 529 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-07-891-942G-8

Query Match 100.0%; Score 83; DB 1; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQ 15  
|||||  
Db 448 DYSYLQSDPDSPDQ 462

RESULT 13  
US-08-370-909-19  
;; Sequence 19, Application US/08370909  
;; Patent No. 5843648  
;; GENERAL INFORMATION:  
;; APPLICANT: ROBBINS, PAUL F.; ROSENBERG,  
;; APPLICANT: STEVEN A.  
;; TITLE OF INVENTION: D15 AND TYROSINASE  
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC  
;; TITLE OF INVENTION: AND THERAPEUTIC METHODS  
;; NUMBER OF SEQUENCES: 23  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
;; STREET: 345 PARK AVENUE  
;; CITY: NEW YORK  
;; STATE: NEW YORK  
;; COUNTRY: USA  
;; ZIP: 10154  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: FLOPPY DISK  
;; COMPUTER: IBM PC COMPATIBLE  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: ASCII  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/370,909  
;; FILING DATE: 10-JAN-1995  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CAROL M. GRUPPI  
;; REGISTRATION NUMBER: 37,341  
;; REFERENCE/DOCKET NUMBER: 2026-4155  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 758-4800  
;; TELEFAX: (212) 751-6849  
;; TELEX: 421792  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 529  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN  
MOLECULE TYPE: PROTEIN

US-08-370-909-19

Query Match 100.0%; Score 83; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15

Db 448 DYSYLQSDPDPSFQD 462

RESULT 14

US-08-504-048-8  
Sequence 8, Application US/08504048  
Patent No. 5843674

GENERAL INFORMATION:

APPLICANT: TAKIMOTO, Hiroyuki

APPLICANT: SUZUKI, Satoshi

APPLICANT: SHIBATA, Kouichi

APPLICANT: MASUI, Shigeki

TITLE OF INVENTION: ANTI-HUMAN TYROSINASE

TITLE OF INVENTION: MONOCLONAL ANTIBODY

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/504,048

FILING DATE:

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: SATOT27.001APC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 714-760-0404

TELEFAX: 714-760-9502

TELEX:

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 529 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

US-08-504-048-8

Query Match 100.0%; Score 83; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15

Db 448 DYSYLQSDPDPSFQD 462

RESULT 15

US-09-341-982-1

Sequence 1, Application US/09341982

Patent No. 6558671

GENERAL INFORMATION:

APPLICANT: SLINGLUFF, Craig L.

APPLICANT: HUNT, Donald F.

APPLICANT: ENGELHARD, Victor H.

APPLICANT: KITTLESEN, David

TITLE OF INVENTION: CYSTEINE-DELETED PEPTIDES RECOGNIZED BY A3-RESTRICTED

TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR

FILE REFERENCE: SLINGLUFF-3B

CURRENT APPLICATION NUMBER: US/09/341,982

CURRENT FILING DATE: 1999-09-20

EARLIER APPLICATION NUMBER: PCT/US98/01592

EARLIER FILING DATE: 1998-01-29

EARLIER APPLICATION NUMBER: 60/037,781

EARLIER FILING DATE: 1997-01-31

NUMBER OF SEQ ID NOS: 104

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 529

TYPE: PRT

ORGANISM: Homo sapiens

US-09-341-982-1

Query Match 100.0%; Score 83; DB 4; Length 529;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15

Db 448 DYSYLQSDPDPSFQD 462

RESULT 16

US-09-169-717E-39

Sequence 39, Application US/09169717E

Patent No. 6667037

GENERAL INFORMATION:

APPLICANT: Ooms, Annie

APPLICANT: DeGiovanni, Gerard

APPLICANT: Morel, Sandra

APPLICANT: Van den Eynde, Benoit

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: Isolater Peptides Which Bind To HLA-B35 Molecules,

TITLE OF INVENTION: Larger Peptides Which Contain These, Nucleic Acid

TITLE OF INVENTION: Molecules Encoding Peptides, And Uses Thereof

FILE REFERENCE: LUD5561

CURRENT APPLICATION NUMBER: US/09/169,717E

CURRENT FILING DATE: 1998-10-09

NUMBER OF SEQ ID NOS: 39

SEQ ID NO 39

LENGTH: 529

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

US-09-169-717E-39

Query Match 100.0%; Score 83; DB 4; Length 529;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15

Db 448 DYSYLQSDPDPSFQD 462

RESULT 17

US-10-011-436-4

Sequence 4, Application US/10011436

Patent No. 6669946

GENERAL INFORMATION:  
APPLICANT: Boon-Falleur, Thierry; Brichard, Vincent; Van Pel, Aline;  
Deplaen, Etienne; Coulie, Pierre; Renauld, Jean Christophe; Wolfel, Lethe, Bernard  
TITLE OF INVENTION: METHOD FOR IDENTIFYING INDIVIDUALS SUFFERING FROM A CELLULAR ABNORMALITY SOME OF WHOSE ABNORMAL CELLS PRESENT LEUKOCYTE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski L.L.P.  
STREET: 901 Pennsylvania Avenue N.W.  
CITY: Washington  
STATE: District of Columbia  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.25inch, 1.44MB storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/011,436  
FILING DATE: 11-Dec-2001  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/511,011  
FILING DATE: 5-AUGUST-1995  
APPLICATION NUMBER: 08/054,714  
FILING DATE: 28-APRIL-1993  
APPLICATION NUMBER: 07/994,928  
FILING DATE: 22-DECEMBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mary Anne Schofield  
REGISTRATION NUMBER: 36,669  
REFERENCE/DOCKET NUMBER: LUD 5299.9 DIV CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 662-0200  
TELEFAX: (202) 662-4643  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 529  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-011-436-4  
Query Match 100.0%; Score 83; DB 4; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYSYLQSDPDPSFQD 15  
DB 448 DYSYLQSDPDPSFQD 462  
RESULT 18  
US-08-540-922D-12  
Sequence 12, Application US/08540922D  
Patent No. 6284476  
GENERAL INFORMATION:  
APPLICANT: Boon-Falleur, Thierry; Brichard, Vincent; Van Pel, Aline; De Plaen, Etienne; Coulie, Pierre; Renauld Jean-Christophe; Wolfel, Thomas; and Lethe, Bernard  
TITLE OF INVENTION: METHOD OF IDENTIFYING INDIVIDUALS SUFFERING FROM A CELLULAR ABNORMALITY SOME OF WHOSE ABNORMAL CELLS PRESENT COMPLEXES OF HUMAN LEUKOCYTE ANTIGEN TYROSINASE DERIVED PEPTIDES, AND METHODS FOR TREATING SAID INDIVIDUALS  
TITLE OF INVENTION: METHOD OF IDENTIFYING INDIVIDUALS SUFFERING FROM A CELLULAR ABNORMALITY SOME OF WHOSE ABNORMAL CELLS PRESENT COMPLEXES OF HUMAN LEUKOCYTE ANTIGEN TYROSINASE DERIVED PEPTIDES, AND METHODS FOR TREATING SAID INDIVIDUALS

NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/540,922D  
FILING DATE: October 11, 1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,714  
FILING DATE: 28 April 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/994,928  
FILING DATE: 22 December 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mary Anne Schofield  
REGISTRATION NUMBER: 36,669  
REFERENCE/DOCKET NUMBER: LUD 5299.5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 537  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-540-922D-12  
Query Match 100.0%; Score 83; DB 3; Length 537;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYSYLQSDPDPSFQD 15  
DB 456 DYSYLQSDPDPSFQD 470  
RESULT 19  
US-07-891-942G-5  
Sequence 5, Application US/07891942G  
Patent No. 5679511  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung Se  
TITLE OF INVENTION: CDNA CLONES FOR HUMAN TYROSINASE AND FOR A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Christopher A. Michaels, Barnard, Brown & Michaels  
STREET: 306 East State Street; Suite 220  
CITY: Ithaca  
STATE: NY  
COUNTRY: USA  
ZIP: 14850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/891,942G  
FILING DATE: 01-JUN-1992  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/915,753  
 FILING DATE: 06-OCT-1986  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/362,847  
 FILING DATE: 07-JUN-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Michaels, Christopher A  
 REGISTRATION NUMBER: 34,390  
 REFERENCE/DOCKET NUMBER: IND1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 607-273-1711  
 TELEFAX: 607-273-2609  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 560 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-891-942G-5

Query Match 100.0%; Score 83; DB 1; Length 560;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDSPQD 15  
 Db 446 DYSYLQSDPDSPQD 460

RESULT 20

US-08-902-516-42  
 Sequence 42, Application US/08902516  
 Patent No. 5891432

GENERAL INFORMATION:

APPLICANT: Soo Hoo, William  
 TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 TITLE OF INVENTION: RESPONSE USING SAME  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMPBELL & FLORES, LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,516  
 FILING DATE: 29-JUL-1997  
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IM 2442  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)535-9001  
 TELEFAX: (619)535-8949

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-902-516-42

Query Match 84.3%; Score 70; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 SYLQSDPDSPQD 15  
 Db 1 SYLQSDPDSPQD 13

Search completed: June 3, 2004, 17:09:00  
 Job time : 24 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:31:31 ; Search time 20 Seconds  
(without alignments)  
72.144 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DYSYLQSDPDSPFQD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2522

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	33.7	12	2	PT0228
2	26	31.3	15	2	IG heavy chain CDR
3	25	30.1	15	2	27K protein A 3.4/
4	25	30.1	15	2	Sf11-glycoprotein
5	24	28.9	12	2	stylar glycoprotei
6	24	28.9	12	2	tachykinin - Afric
7	23	27.7	9	2	Sz-glycoprotein -
8	21	25.3	5	2	exotoxin A - Strep
9	21	25.3	10	2	blood cell protein
10	21	25.3	11	2	polygalacturonase
11	21	25.3	11	2	uperolein - frog (
12	21	25.3	14	2	physalaemin - frog
13	21	25.3	14	2	unidentified 27.2K
14	21	25.3	15	2	dystrophin-asocia
15	20	24.1	7	2	T-cell receptor al
16	20	24.1	8	2	calliferramide 11
17	20	24.1	11	2	glucose-6-phosphat
18	20	24.1	11	2	substance P-like p
19	20	24.1	12	2	kassinin-like pept
20	20	24.1	12	2	cytokinin-binding
21	20	24.1	12	2	hemocyanin 1 - gre
22	20	24.1	14	2	exonuclease ABC c
23	20	24.1	15	2	agrin - electric r
24	20	24.1	15	2	gallbladder stone
25	19	22.9	6	2	T-cell receptor be
26	19	22.9	9	2	IG heavy chain CDR
27	19	22.9	10	2	Gastric juice pept
28	19	22.9	10	2	hementin (EC 3.4.-
29	19	22.9	10	2	mosact - sea urchi
			11	2	kassinin-like pept
			11	2	B60409

30	19	22.9	11	2	S18385
31	19	22.9	12	2	S10059
32	19	22.9	12	2	PA0047
33	19	22.9	12	2	S74144
34	19	22.9	13	2	H56046
35	19	22.9	14	2	S39931
36	19	22.9	14	2	S39930
37	19	22.9	15	2	PQ0192
38	19	22.9	15	2	S29485
39	19	22.9	15	2	E49037
40	18	21.7	7	2	A60139
41	18	21.7	8	2	S68325
42	18	21.7	10	1	GMROL2
43	18	21.7	10	2	PH0113
44	18	21.7	10	2	B60656
45	18	21.7	11	1	GMROL

NADP-cytochrome P4  
tachykinin - Afric  
protein QA100045 -  
aggreccan - bovine  
urinary tract ston  
S-allele-associate  
stylar glycoprotei  
GTP-binding protei  
TCR delta chain V-  
fatty-acid synthas  
blood cell protein  
leucosulfakinin-II  
alpha-amylase (EC  
leucosulfakinin II  
leucosulfakinin -

#### ALIGNMENTS

##### RESULT 1

PT0228

IG heavy chain CDR3 region (clone 1-112) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0228

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0228

A:Molecule type: DNA

A:Residues: 1-12 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 33.7%; Score 28; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YLQSDPD 11

DB 3 YVRDSSPE 10

##### RESULT 2

PS0185

27K protein A 3.4/5 - rice (fragment)

C:Species: Oryza sativa (rice)

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 24-Feb-1995

C:Accession: PS0185

R:Kamo, M.; Tsugita, A.

submitted to JIPID, June 1991

A:Reference number: PS0184

A:Accession: PS0185

A:Molecule type: Protein

A:Residues: 1-15 <KAM>

Query Match 31.3%; Score 26; DB 2; Length 15;

Best Local Similarity 55.6%; Pred. No. 4.1e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YLQSDPD 12

DB 4 YIVDVAPDS 12

##### RESULT 3

PQ0195

Sf11-glycoprotein - Persian tobacco (fragment)

N:Alternate names: Sf1-glycoprotein

C:Species: Nicotiana glauca (Persian tobacco)

C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 03-Aug-1998  
 C;Accession: PQ0195; PQ0173  
 R;Mau, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Simpson, R.; J.P.; Crawford, R.J.; Clarke, A.E.  
 Planta 169, 184-191, 1986  
 A;Title: Style proteins of a wild tomato (Lycopersicon peruvianum) associated with expression of self-incompatibility  
 A;Reference number: PQ0192  
 A;Accession: PQ0195  
 A;Molecule type: protein  
 A;Residues: 1-15 <MAU>  
 A;Experimental source: style  
 R;Jahnen, W.; Batterham, M.P.; Clarke, A.E.; Moritz, R.L.; Simpson, R.  
 Plant Cell 1, 493-499, 1989  
 A;Title: Identification, isolation, and N-terminal sequencing of style glycoproteins associated with self-incompatibility  
 A;Reference number: PQ0173; PMID:2535548  
 A;Accession: PQ0173  
 A;Molecule type: protein  
 A;Residues: 1-15 <JAH>  
 A;Experimental source: style  
 C;Comment: This protein is involved in self-incompatibility of flowering plants.  
 C;Superfamily: Enterobacter ribonuclease  
 C;Keywords: glycoprotein

Query Match 30.1%; Score 25; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYIQ 6  
 | : |||  
 Db 1 DFYILQ 6

## RESULT 4

PQ0193  
 stylar glycoprotein 3 - Peruvian tomato (fragment)  
 N;Alternate names: S3-glycoprotein  
 C;Species: Lycopersicon peruvianum (Peruvian tomato)  
 C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 23-Aug-1997  
 C;Accession: PQ0193; A28819  
 R;Mau, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Simpson, R.; J.P.; Crawford, R.J.; Clarke, A.E.  
 Planta 169, 184-191, 1986  
 A;Title: Style proteins of a wild tomato (Lycopersicon peruvianum) associated with expression of self-incompatibility  
 A;Reference number: PQ0192  
 A;Accession: PQ0193  
 A;Molecule type: protein  
 A;Residues: 1-15 <MAU>  
 A;Experimental source: style, strain Mill  
 R;Anderson, M.A.; Cornish, E.C.; Mau, S.L.; Williams, E.G.; Hoggart, R.; Atkinson, A.; B.

Nature 321, 38-44, 1986  
 A;Title: Cloning of cDNA for a stylar glycoprotein associated with expression of self-incompatibility  
 A;Reference number: A28819  
 A;Accession: A28819  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-15 <AND>  
 C;Keywords: glycoprotein

Query Match 30.1%; Score 25; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYIQ 6  
 | : |||  
 Db 1 DFYILQ 6

## RESULT 5

S07436  
 tachykinin - African tree frog (Kassina maculata)  
 N;Alternate names: hylambatin  
 C;Species: Kassina maculata  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 02-Sep-2000  
 C;Accession: S07436

R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.  
 Biomed. Res. 2, 613-617, 1981  
 A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in tachykinin family  
 A;Reference number: S07436  
 A;Accession: S07436  
 A;Molecule type: protein  
 A;Residues: 1-12 <YAS>  
 A;Experimental source: skin  
 A;Note: the source is designated as Hylambates maculatus  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
 F12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 28.9%; Score 24; DB 2; Length 12;  
 Best Local Similarity 80.0%; Pred. No. 6.7e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 DPDSF 13  
 ||| : |||  
 Db 4 DPDRF 8

## RESULT 6

PQ0194  
 Sz-glycoprotein - Persian tobacco (fragment)  
 C;Species: Nicotiana glauca (Persian tobacco)  
 C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 03-Mar-1995  
 C;Accession: PQ0194  
 R;Mau, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Simpson, R.; J.P.; Crawford, R.J.; Clarke, A.E.

Planta 169, 184-191, 1986  
 A;Title: Style proteins of a wild tomato (Lycopersicon peruvianum) associated with expression of self-incompatibility  
 A;Reference number: PQ0192  
 A;Accession: PQ0194  
 A;Molecule type: protein  
 A;Residues: 1-15 <MAU>  
 A;Experimental source: style  
 C;Keywords: glycoprotein

Query Match 28.9%; Score 24; DB 2; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 8.6e+02;  
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DYSYIQSDPDSF 13  
 ||| : |||  
 Db 3 DYNQLVLTXPASF 15

## RESULT 7

A60108  
 exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)  
 N;Alternate names: blastogen A; scarlet fever toxin  
 C;Species: Streptococcus pyogenes  
 C;Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 07-Feb-1997  
 C;Accession: A60108  
 R;Schlievert, P.M.; Gray, E.D.  
 Infect. Immun. 57, 1865-1867, 1989  
 A;Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blastogen A  
 A;Reference number: A60108; PMID:89254013; PMID:2498210  
 A;Accession: A60108  
 A;Molecule type: protein  
 A;Residues: 1-9 <SCH>  
 C;Keywords: exotoxin

Query Match 27.7%; Score 23; DB 2; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 QDSDF 10  
 ||| : |||  
 Db 1 QDPDP 5

## RESULT 8



S68326  
blood cell protein B - Ascidia ceratodes (fragment)  
N;Alternate names: Abcp-B  
C;Species: Ascidia ceratodes  
C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 11-Jun-1999  
C;Accession: S68326  
R;Taylor, S.W.; Ross, M.M.; Waite, J.H.  
Arch. Biochem. Biophys. 324, 228-240, 1995  
A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from the  
A;Reference number: S68325; MUID:96132650; PMID:8554314  
A;Accession: S68326  
A;Molecule type: protein  
A;Residues: 1-5 <YAY>  
F;1/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental  
F;4/Modified site: 3',4',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 25.3%; Score 21; DB 2; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSY 4  
||:|  
Db 1 DYAY 4

RESULT 9  
S62880  
polysaccharuronase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)  
C;Species: Aspergillus sp.  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C;Accession: S62880  
R;Stratilova, B.; Dzurava, M.; Markovic, O.; Joernvall, H.  
FEBS Lett. 382, 164-166, 1996  
A;Title: An essential tyrosine residue of Aspergillus polysaccharuronase.  
A;Reference number: S62880; MUID:96196586; PMID:8612742  
A;Accession: S62880  
A;Molecule type: protein  
A;Residues: 1-10 <STR>  
C;Keywords: glycosidase; hydrolase  
F;4/Active site: Tyr #status predicted

Query Match 25.3%; Score 21; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSY 4  
||:|  
Db 1 DYAY 4

RESULT 10  
S07203  
uperolein - frog (Uperoleia marmorata)  
C;Species: Uperoleia marmorata  
C;Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000  
C;Accession: S07203  
R;Anastasi, A.; Erspamer, V.; Eudean, R.  
Experientia 31, 394-395, 1975  
A;Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin  
A;Reference number: S07203; MUID:75131227; PMID:1120493  
A;Accession: S07203  
A;Molecule type: protein  
A;Residues: 1-11 <ANA>  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 25.3%; Score 21; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 DPDSF 13

Db 3 DPNAF 7  
||:|  
||:|

RESULT 11  
S07201  
physalaemin - frog (Physalaemus fuscumaculatus)  
C;Species: Physalaemus fuscumaculatus  
C;Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000  
C;Accession: S07201  
R;Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.  
Experientia 20, 489-490, 1964  
A;Title: Structure and pharmacological actions of physalaemin, the main active polypept-  
A;Reference number: S07201; MUID:66076612; PMID:5857249  
A;Accession: S07201  
A;Molecule type: protein  
A;Residues: 1-11 <ERS>  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 25.3%; Score 21; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 SDPSF 13  
||:|  
Db 2 ADPNKF 7

RESULT 12  
PC7079  
unidentified 27.2K protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C;Accession: PC7079  
R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
Electrophoresis 21, 1853-1871, 2000  
A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of  
A;Reference number: PC7072  
A;Accession: PC7079  
A;Molecule type: protein  
A;Residues: 1-14 <TSU>  
A;Experimental source: strain C57BL/6Cr Slc, male; brain, striatum  
C;Keywords: brain

Query Match 25.3%; Score 21; DB 2; Length 14;  
Best Local Similarity 27.3%; Pred. No. 2.4e+03;  
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 YSYLQSDSPDS 12  
||:|  
Db 2 KYVNVKKEQES 12

RESULT 13  
PN0665  
dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999  
C;Accession: PN0665  
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.  
J. Biochem. 114, 634-639, 1993  
A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained  
A;Reference number: PN0662; MUID:94156881; PMID:8113213  
A;Accession: PN0665  
A;Molecule type: protein  
A;Residues: 1-15 <YOS>  
A;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.  
C;Keywords: glycoprotein; skeletal muscle

Query Match 25.3%; Score 21; DB 2; Length 15;

Best Local Similarity 36.4%; Pred. No. 2.6e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YSYLQSDPDPS 12  
| | | | |  
Db 1 YTPLLDXXPNA 11

RESULT 14  
PH0784  
T-cell receptor alpha chain (F1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PH0784  
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.  
A:Reference number: PH0746; MUID:92078846; PMID:1836010  
A:Accession: PH0784  
A:Molecule type: mRNA  
A:Residues: 1-15 <CAS>  
A:Cross-references: EMBL:X60885  
A:Experimental source: T lymphocyte  
C:Keywords: T-cell receptor

Query Match 25.3%; Score 21; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 SDPDSF 13  
| | | | |  
Db 4 SDPSNY 9

RESULT 15  
B44787  
calliphoramide 11 - bluebottle fly (Calliphora vomitoria)  
C:Species: Calliphora vomitoria  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
C:Accession: B44787  
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
A:Reference number: A41978; MUID:92196111; PMID:1549595  
A:Accession: B44787  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <DUV>  
C:Keywords: amidated carboxyl end; neuropeptide  
F;7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.1%; Score 20; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 PDSF 13  
| | | | |  
Db 1 PDNF 4

Search completed: June 3, 2004, 15:35:16  
Job time : 21 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:27:56 ; Search time 11.5 seconds  
(without alignments)  
71.005 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DYSVLQSDPDSFQD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 801

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	24	28.9	12	TKN2_KASMA	P08614 kassina mac
2	23	27.7	10	CATB_SHEEP	P83205 ovine aries
3	23	27.7	13	GER1_HORVU	P28525 hordeum vul
4	23	27.7	13	GER2_HORVU	P28526 hordeum vul
5	23	27.7	15	ECDA_LYMDI	P80938 lymantria d
6	22	26.5	11	TKN1_UPEIN	P82026 uperoleia i
7	21	25.3	11	TKN1_UPERU	P08612 uperoleia r
8	21	25.3	11	TKN1_PHYFU	P08615 physalaemus
9	20	24.1	7	FARB_CALVO	P41866 calliphora
10	20	24.1	11	TKN2_PSEGU	P42987 pseudophryn
11	20	24.1	11	TKN2_UPERU	P08616 uperoleia r
12	20	24.1	11	TKN4_PSEGU	P42989 pseudophryn
13	20	24.1	12	HCY1_CARMA	P83176 carcinus ma
14	20	24.1	13	ECDE_LYMDI	P80941 lymantria d
15	20	24.1	13	LPFA_FORGI	P81411 porphyromon
16	19	22.9	10	GAJU_HUMAN	P01358 homo sapien
17	19	22.9	10	MOSQ_CLYJA	P19962 clypeaster
18	19	22.9	10	PRCK_FASHE	P80525 fasciola he
19	19	22.9	10	UH05_RAT	P56573 rattus norv
20	19	22.9	10	UPA9_HUMAN	P30095 homo sapien
21	19	22.9	11	TKN1_PSEGU	P42986 pseudophryn
22	19	22.9	12	TKN1_KASMA	P08613 kassina mac
23	19	22.9	14	GLGS_SPIOI	P55235 spinacia ol
24	18	21.7	8	AL16_CARMA	P81819 carcinus ma
25	18	21.7	8	FAR1_PANRE	P41872 panagrellus
26	18	21.7	9	NSX1_SARBU	P41492 sarcophaga
27	18	21.7	10	AMPN_HELAM	P81731 helicoverpa
28	18	21.7	10	LSK2_LEUMA	P09039 leucophaea
29	18	21.7	11	LSK1_LEUMA	P04428 leucophaea
30	18	21.7	11	LSKP_PERAM	P36885 periplaneta
31	18	21.7	11	TKNA_RANCA	P22688 rana catesbe
32	18	21.7	12	LOSK_LOCMI	P47733 locusta mig
33	18	21.7	12	ULAL_MOUSE	P99032 mus musculu

34	18	21.7	14	1	NSK2_SARBU	P41493 sarcophaga
35	18	21.7	15	1	VORA_METTM	P80907 methanobact
36	17	20.5	7	1	ALL4_CARMA	P81807 carcinus ma
37	17	20.5	9	1	LPCA_STRAU	P36884 staphylococ
38	17	20.5	9	1	UF02_MOUSE	P38640 mus musculu
39	17	20.5	12	1	CKA1_CONIM	P50983 conus imper
40	17	20.5	13	1	UN12_CLOPA	P81353 clostridium
41	17	20.5	15	1	AVP2_CAVPO	P83508 cavia porce
42	17	20.5	15	1	UC06_MAIZE	P80612 zea mays (m
43	16	19.3	5	1	PSK_DAUCA	P58261 daucus caro
44	16	19.3	8	1	ALL3_CYDPO	P82154 cydia pomon
45	16	19.3	9	1	MOSF_CLYJA	P19853 clypeaster

## ALIGNMENTS

RESULT 1  
TKN2\_KASMA STANDARD; PRT; 12 AA.  
AC P08614;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hylambatin.  
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;  
OC Kassina.  
OX NCBI\_TaxID=8414;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;  
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and  
RT hylambatin, in the skin of the African rhacophorid frog Hylambates  
RT maculatus.";  
RL Biomed. Res. 2:613-617(1981).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; S07436; S07436. Tachy Neurokinin.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 12  
FT SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;  
SQ  
Query Match 28.9%; Score 24; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 DPDSF 13  
Db 4 DPDRF 8

RESULT 2  
CATB\_SHEEP STANDARD; PRT; 10 AA.  
ID CATB\_SHEEP  
AC P83205;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (fragment).  
GN CTSP.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22394055; PubMed=12506352;  
 RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,  
 RA Mboko H.B., Beckers J.-F.M.P.;  
 RT "Isolation and partial characterization of three pregnancy-associated  
 RT glycoproteins from the ewe placenta."  
 RL Mol. Reprod. Dev. 64:199-206 (2003).  
 CC -!- FUNCTION: Thiol protease which is believed to participate in  
 CC intracellular degradation and turnover of proteins. Has also been  
 CC implicated in tumor invasion and metastasis.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in  
 CC small molecule substrates (thus differing from cathepsin L). In  
 CC addition to being an endopeptidase, shows peptidyl-dipeptidase  
 CC activity, liberating C-terminal dipeptides.  
 CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked  
 CC by a disulfide bond (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).  
 CC -!- SIMILARITY: Belongs to peptidase family C1.  
 DR InterPro; IPR00169; SHROT acsite.  
 DR PROSITE; PS00640; THIOLEPROTEASE ASN; PARTIAL.  
 DR PROSITE; PS00139; THIOLEPROTEASE CVS; PARTIAL.  
 DR PROSITE; PS00639; THIOLEPROTEASE HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;  
 Query Match 27.7%; Score 23; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 PDSF 13  
 Db 2 PDSF 5  
 RESULT 3  
 GERL\_HORVU STANDARD; PRT; 13 AA.  
 ID GERL\_HORVU  
 AC P28525;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GS1 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Hukman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 RT stress."  
 RL Plant Physiol. 97:366-374 (1991).  
 CC -!- FUNCTION: May play a role in altering the properties of cell walls  
 CC during germinative growth.  
 CC -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)  
 CC (By similarity).  
 CC -!- SIMILARITY: Belongs to the germin family.  
 DR InterPro; IPR001929; Germin.  
 DR PROSITE; PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT NON TER 10 10  
 SQ SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7B6D7 CRC64;  
 Query Match 27.7%; Score 23; DB 1; Length 13;  
 Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 9 DPDSFQD 15  
 Db 2 DPSPLOD 8  
 RESULT 5  
 ECDA\_LYMDI STANDARD; PRT; 15 AA.  
 ID ECDA\_LYMDI  
 AC P80338;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Testis ecdysiotropin peptide A (TE).  
 OS Lymantria dispar (Gypsy moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;

DR PROSITE; PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT UNSURE 10 10  
 FT NON TER 13 13  
 SQ SEQUENCE 13 AA; 1470 MW; 43FB589AA3B7B6D7 CRC64;  
 Query Match 27.7%; Score 23; DB 1; Length 13;  
 Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 9 DPDSFQD 15  
 Db 2 DPSPLOD 8  
 RESULT 4  
 GER2\_HORVU STANDARD; PRT; 13 AA.  
 ID GER2\_HORVU  
 AC P28526;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GS2 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Hukman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 RT stress."  
 RL Plant Physiol. 97:366-374 (1991).  
 CC -!- FUNCTION: May play a role in altering the properties of cell walls  
 CC during germinative growth.  
 CC -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.  
 CC -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in the  
 CC mature region, but not in the tip. Not detected in leaves.  
 CC -!- INDUCTION: Increased by salt stress in roots and decreased by salt  
 CC stress in coleoptile.  
 CC -!- PTM: Glycosylated.  
 CC -!- SIMILARITY: Belongs to the germin family.  
 DR InterPro; IPR001929; Germin.  
 DR PROSITE; PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT NON TER 10 10  
 SQ SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7B6D7 CRC64;  
 Query Match 27.7%; Score 23; DB 1; Length 13;  
 Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 9 DPDSFQD 15  
 Db 2 DPSPLOD 8  
 RESULT 5  
 ECDA\_LYMDI STANDARD; PRT; 15 AA.  
 ID ECDA\_LYMDI  
 AC P80338;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Testis ecdysiotropin peptide A (TE).  
 OS Lymantria dispar (Gypsy moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;

```

OC Lymantriidae; Lymantria.
OX NCBI_TaxID=131123;
RN [1]
RP SEQUENCE.
RX MEDLINE=97387807; PubMed=9243792;
RA Leeb R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
gonadotropin isolated from brains of Lymantria dispar pupae."
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes
of larvae and pupae.
SQ SEQUENCE 15 AA; 1712 MW; 12E8D8246B74EE26 CRC64;

Query Match 27.7%; Score 23; DB 1; Length 15;
Best Local Similarity 44.4%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DYSYLQDS 9
Db 7 EYEPLNDAD 15

RESULT 6
TKN1 UPEIN STANDARD; PRT; 11 AA.
AC P82026;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperin 1.1.
OS Uperoleia inundata (Bloodplains toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the Australian
bloodplains toadlet Uperoleia inundata."
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
evoke behavioral responses, are potent vasodilators and
secreteagogues, and contract (directly or indirectly) many smooth
muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy. Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 26.5%; Score 22; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SDPDSF 13
Db 2 ADPNAP 7

RESULT 7
TKN1 UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspaner V., Edean R.;
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
in the skin of Uperoleia rugosa and Uperoleia marmorata."
RL Experientia 31:394-395(1975).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
evoke behavioral responses, are potent vasodilators and
secreteagogues, and contract (directly or indirectly) many smooth
muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy. Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 25.3%; Score 21; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 DPDSF 13
Db 3 DPNAP 7

RESULT 8
TKN PHYFU STANDARD; PRT; 11 AA.
AC P08615;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Physalaemin.
OS Physalaemus fuscumaculatus (Neotropical frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Leptodactylinae; Physalaemus.
OX NCBI_TaxID=8378;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=66076612; PubMed=5857249;
RA Erspaner V., Anastasi A., Bertaccini G., Cei J.M.;
RT "Structure and pharmacological actions of physalaemin, the main
active polypeptide of the skin of Physalaemus fuscumaculatus."
RL Experientia 20:489-490(1964).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
evoke behavioral responses, are potent vasodilators and
secreteagogues, and contract (directly or indirectly) many smooth
muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.

```

```

CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S07201; S07201.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 11 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1283 MW; 3293693859C33457 CRC64;

Query Match 25.3%; Score 21; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 DPDSF 13
DB 2 ADPNKF 7

RESULT 9
FARB CALVO STANDARD; PRT; 7 AA.
AC P41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 11.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
SEQUENCE.
RP TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
CC PIR; B44787; B44787.
DR Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 926 MW; 69D40699C44AB700 CRC64;

Query Match 24.1%; Score 20; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 PDNF 13
DB 1 PDNF 4

RESULT 10
TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
DE Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]

```

```

RP SEQUENCE.
RX TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; C60409; C60409.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SMO0203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 11 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9C1AB7 CRC64;

Query Match 24.1%; Score 20; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 DPDSF 13
DB 3 NPDEF 7

RESULT 11
TKN2_UPERU STANDARD; PRT; 11 AA.
AC P08616;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rugosauperolein II ((Lys5,Thr6)physalaemin).
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
SEQUENCE.
RP TISSUE=Skin secretion;
RX MEDLINE=80223080; PubMed=7389029;
RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
RT "Physalaemin- and bombesin-like peptides in the skin of the
RT Australian leptodactylid frog Uperoleia rugosa.";
RL Chem. Pharm. Bull. 28:689-695(1980).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 11 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1270 MW; 3293693859DIA327 CRC64;

```

Query Match 24.1%; Score 20; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 DPDSDF 13  
DB 2 ADPKTF 7

RESULT 12  
TKN4 PSEGU  
ID TKN4 PSEGU STANDARD; PRT; 11 AA.  
AC P42989;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P-like peptide I (PG-SPI).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP TISSUE=Skin secretion;  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; E60409; E60409.  
DR InterPro; IPR020400; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 24.1%; Score 20; DB 1; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 DPDSF 13  
DB 3 NDEF 7

RESULT 13  
HCY1 CARMA  
ID HCY1 CARMA STANDARD; PRT; 12 AA.  
AC P83176;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hemocyanin subunit 1 (fragment).  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunodea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]

RP SEQUENCE.  
RC TISSUE=Hemolymph;  
RX MEDLINE=90151075; PubMed=2620501;  
RA Neuteboom B., Sierdsema S.J., Beintema J.J.;  
RT "The relationship between N-terminal sequences and immunological  
RT characterization of crustacean hemocyanins.";  
RL Comp. Biochem. Physiol. 94B:587-592(1989).  
CC -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers  
CC occurring freely dissolved in the hemolymph of many mollusks and  
CC arthropods.  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- TISSUE SPECIFICITY: Hemolymph.  
CC -!- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin  
CC subfamily.  
DR PIR; C60529; C60529.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0005344; P:oxygen transporter activity; IDA.  
DR GO; GO:0015671; P:oxygen transport; TAS.  
KW Transport; Oxygen transport; Copper; Hemolymph.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1237 MW; 89936EF6E2B5A2D5 CRC64;

Query Match 24.1%; Score 20; DB 1; Length 12;  
Best Local Similarity 57.1%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 DPDSFQD 15  
DB 2 DPASVSD 8

RESULT 14  
ECDE LYMDI  
ID ECDE LYMDI STANDARD; PRT; 13 AA.  
AC P80941;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Testis ecdysiotropin peptide E (TE).  
OS Lymantria dispar (Gypsy moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Lymantriidae; Lymantria.  
OX NCBI\_TaxID=13123;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=97387807; PubMed=9243792;  
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,  
RA Bell R.A.;  
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a  
RT gonadotropin isolated from brains of Lymantria dispar pupae.";  
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).  
CC -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of  
CC larvae and pupae.  
SQ SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;

Query Match 24.1%; Score 20; DB 1; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 DSDPDS 12  
DB 4 DPNPDT 9

RESULT 15  
LPAA PORGI  
ID LPAA PORGI STANDARD; PRT; 13 AA.  
AC P81411;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Lipid-A-associated protein (Fragment).  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI\_TaxID=837;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W50;  
EX MEDLINE=95061194; PubMed=9846737;  
RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,  
RA Curtis M., Henderson B., Tabona P.;  
RT "A lipid A-associated protein of Porphyromonas gingivalis, derived  
RT from the haemagglutinating domain of the RI protease gene family, is  
RT a potent stimulator of interleukin 6 synthesis.";  
RL Microbiology 144:3019-3026(1998).  
CC -!- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID  
CC THAT ANCHORS THE LIPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE  
CC CELL.  
FT VARIANT 12 12 G -> F.  
FT NON TER 13 13  
SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF63AB7 CRC64;  
Query Match 24.1%; Score 20; DB 1; Length 13;  
Best Local Similarity 40.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
OY 6 QDSDPDSFQD 15  
Db 2 QGDNFDKJTD 11

Search completed: June 3, 2004, 15:33:51  
Job time : 11 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:31:01 ; Search time 38 Seconds  
(without alignments)  
124.547 Million cell

Title: US-08-533-895A-39\_COPY\_448\_462  
perfect score: 83  
sequence: 1 DYSXL0DSDPDSFOD 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3954

```
Minimum DB seq length: 0
Maximum DB seq length: 15
```

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

```
STREMBL 25:*
1:  sp_archaea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phase:*
10: sp_plant:*
11: sp_rickettsia:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriophage:*
17: sp_archaeal:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMARTES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	25.5	30.7	15	4	Q9UC04	Q9UC04 homo sapien
2	25	30.1	15	10	Q9S8X0	Q9S8X0 nicotiana a
3	25	30.1	15	10	Q40563	Q40563 nicotiana t
4	24	28.9	14	4	Q14342	Q14342 homo sapien
5	22	26.5	8	12	Q9WJ33	Q9WJ33 pseudorabie
6	22	26.5	13	4	Q9UEE2	Q9UEE2 homo sapien
7	22	26.5	13	4	Q9UEE3	Q9UEE3 homo sapien
8	22	26.5	15	6	Q9TR40	Q9TR40 bos taurus
9	22	26.5	15	6	Q9TQ09	Q9TQ09 bos taurus
10	21	25.3	8	4	Q9HC00	Q9HC00 homo sapien
11	21	25.3	9	4	Q9BYF9	Q9BYF9 homo sapien
12	21	25.3	11	2	P96319	P96319 desulfofibr
13	21	25.3	12	6	Q9TQY4	Q9TQY4 bos taurus
14	21	25.3	13	2	Q9R7D6	Q9R7D6 clostridium
15	21	25.3	13	12	Q9IBN1	Q9IBN1 influenza a
16	21	25.3	14	12	Q84708	Q84708 porcine epi

## ALIGNMENTS

## RESULT 1

Q9UCC4  
ID Q9UCC4  
PRT: 15 AA.

AC	
DT	O9UCG4:
DT	01-MAY-2000 (TRENBUrel. 13, Created)
DT	01-MAY-2000 (TRENBUrel. 13, Last sequence update)
DE	01-JUN-2000 (TRENBUrel. 14, Last annotation update)
DE	33 kDa heparin-RELEASABLE protein (fragment).
DE	Homo sapiens (Human).
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI TaxID=9606
OX	

Query Match	30.7%;	Score	25.5;	DB	4;	Length	15;
Best Local Similarity	33.3%;	Pred. No.	1.3e+03;				
Matches	5;	Conservative	4;	Mismatches	5;	Indels	

RESULT 2

RESULTS	PRELIMINARY	PPT.	15 AA
Q9S8X0	TD Q9S8X0		

Q9ubk0 homo sapien  
Q93o46 homo sapien  
Q9ucho homo sapien  
Q9hz79 bos taurus  
P93515 arabidopsis  
Q94562 nicotiana t  
Q8c129 mus musculus  
Q97605 squash leaf  
Q97606 squash leaf  
Q9gwu0 mus musculus  
Q9urp1 sus scrofa  
Q9trp9 bos taurus  
P93516 arabidopsis  
Q98936 nicotiana t  
Q90403 discopyge o  
P79484 homo sapien  
Q9gwme rattus norv  
Q85ih3 plestrum m  
Q9gw04 mus sp. pl  
Q9r420 rhodobacter  
Q9umy6 homo sapien  
Q42223 arabidopsis  
Q8ciw3 mus musculus  
P83529 lactobacilli  
P90391 tomato yell  
Q9oy93 gallus gall  
Q8rd48 homo sapien  
Q9ueta4 homo sapien  
Q90gd1 human immun

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4087;  
RN [1]  
RP SEQUENCE.

RA MEDLINE=92404717; PubMed=2535548;  
RX Jahnhen W., Batterham M.P., Clarke A.E., Moritz R.L., Simpson R.J.;  
RT "Identification, isolation, and N-terminal sequencing of style  
RT glycoproteins associated with self-incompatibility in Nicotiana  
RT glabra";  
RL Plant Cell 1:493-499 (1989).  
DR PIR; PQ0195; PQ0195.  
DR GO; GO:0004521; F-endoribonuclease activity; IEA.  
DR GO; GO:0003723; F-RNA binding; IEA.  
DR InterPro; IPR001568; RNase T2.  
DR Pfam; PF00445; ribonuclease\_T2; 1.  
SQ SEQUENCE 15 AA; 1829 MW; D9EDB6F55B262D66 CRC64;

Query Match 30.1%; Score 25; DB 10; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYLQ 6  
|: |||  
Db 1 DPEYLQ 6

RESULT 3  
Q40563 PRELIMINARY; PRT; 15 AA.  
ID Q40563;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Small ras-related protein (Fragment).  
GN RAN-B2.  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SR1;  
RX MEDLINE=95078947; PubMed=7987414;  
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;  
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46  
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding  
RT protein";  
RL Plant J. 6:555-565 (1994).  
DR EMBL; LI6788; AAA73565.1; -.  
DR GO; GO:0005525; F-GTP binding; IEA.  
KW GTP-binding.  
FT NON\_TER 1 1  
SQ SEQUENCE 15 AA; 1604 MW; 9A57F48F1FFFFFAF CRC64;

Query Match 30.1%; Score 25; DB 10; Length 15;  
Best Local Similarity 40.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 LQSDPDPSFQ 14  
|: |||: :  
Db 6 LPDDDDAEFE 15

RESULT 4  
Q14342 PRELIMINARY; PRT; 14 AA.  
ID Q14342  
AC Q14342;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE FYN protein (Fragment).  
GN FYN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88234523; PubMed=3287380;  
RA Kawakami T., Kawakami Y., Aaronson S.A., Robbins K.C.;  
RT "Acquisition of transforming properties by FYN, a normal SRC-related  
RT human gene";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874 (1988).  
DR EMBL; M20285; AAA52492.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 14 AA; 1825 MW; 4F3C8DD2E972BA17 CRC64;

Query Match 28.9%; Score 24; DB 4; Length 14;  
Best Local Similarity 54.5%; Pred. No. 2.2e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 YLQSDPDPSFQ 14  
|: |||  
Db 2 YLQSFLEDFQ 12

RESULT 5  
Q9WJ33 PRELIMINARY; PRT; 8 AA.  
ID Q9WJ33;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Suid herpesvirus 1 putative UL47 and UL46 genes and partial gb  
DE (Fragment).  
GN GB.  
OS Pseudorabies virus (strain Kaplan) (PRV).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicelloviruses.  
OX NCBI\_TaxID=33703;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Kaplan;  
RX MEDLINE=99239778; PubMed=10225272;  
RA Bras F., Dezelee S., Simonet B., Nguyen X., Vende P., Flamand A.,  
RA Masse M.J.;  
RT "The left border of the genomic inversion of pseudorabies virus  
RT contains genes homologous to the UL46 and UL47 genes of Herpes Simplex  
RT Virus type 1, but no UL45 gene";  
RL Virus Res. 60:29-40 (1999).  
DR EMBL; AJ010303; CAA09075.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 8 AA; 875 MW; 262DDAB76AAB05BB CRC64;

Query Match 26.5%; Score 22; DB 12; Length 8;  
Best Local Similarity 42.9%; Pred. No. 1e+06;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 QSDPDPS 12  
|: |||: 7  
Db 1 ESEDPDA 7

RESULT 6  
Q9UEE2 PRELIMINARY; PRT; 13 AA.  
ID Q9UEE2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE ERGB transcription factor (Fragment).  
GN FL11.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1] NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;  
 RT "Molecular analysis on the breakpoint region of a t(11:22)  
 RL translocation in Ewing's sarcoma";  
 DR Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AB012625; BAA32806.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1541 MW; 2C677798CB566AB7 CRC64;

Query Match 26.5%; Score 22; DB 4; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 4.4e+03;  
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 QSDPDSFQ 14  
 Db 2 QRQPDYQ 10

## RESULT 7

Q9UEE3 PRELIMINARY; PRT; 13 AA.  
 AC Q9UEE3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE ERGB transcription factor (Fragment).  
 GN FL11.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;  
 RT "Molecular analysis on the breakpoint region of a t(11:22)  
 RL translocation in Ewing's sarcoma";  
 DR Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB012624; BAA32805.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1529 MW; 629F6FCA649A5BB CRC64;

Query Match 26.5%; Score 22; DB 4; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 4.4e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYLQDS 8  
 Db 2 SYLRES 7

## RESULT 8

Q9TR40 PRELIMINARY; PRT; 15 AA.  
 AC Q9TR40;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Glutamate dehydrogenase isoform II (EC 1.4.1.2) (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RA Cho S.W., Lee J., Choi S.Y.;  
 RT MEDLINE=96061967; PubMed=7588764;  
 RX "the human phosphodiesterase PDE10A gene. Genomic organization and  
 evolutionary relatedness with other PDEs containing GAF domains.";

RT "Two soluble forms of glutamate dehydrogenase isoproteins from bovine  
 RL brain";  
 RL Eur. J. Biochem. 233:340-346(1995).  
 DR GO; GO:0004352; F:glutamate dehydrogenase activity; IEA.  
 SQ SEQUENCE 15 AA; 1724 MW; 65F7CD91023AF925 CRC64;

Query Match 26.5%; Score 22; DB 6; Length 15;  
 Best Local Similarity 33.3%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 6 QSDPDSFQ 14  
 Db 7 REDDPNFFK 15

## RESULT 9

Q9TQ09 PRELIMINARY; PRT; 15 AA.  
 AC Q9TQ09;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Glutamate dehydrogenase isoform I (EC 1.4.1.2) (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96061967; PubMed=7588764;  
 RA Cho S.W., Lee J., Choi S.Y.;  
 RT "Two soluble forms of glutamate dehydrogenase isoproteins from bovine  
 RL brain";  
 RL Eur. J. Biochem. 233:340-346(1995).  
 RN [2]  
 RP SEQUENCE.

Query Match 26.5%; Score 22; DB 6; Length 15;  
 Best Local Similarity 33.3%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 6 QSDPDSFQ 14  
 Db 7 REDDPNFFK 15

## RESULT 10

Q9HCQ0 PRELIMINARY; PRT; 8 AA.  
 AC Q9HCQ0;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Phosphodiesterase 10A7 (PDE10A7) (Fragment).  
 GN HSPDE10A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20453115; PubMed=10998054;  
 RX Fujishige K., Kotera J., Yuasa K., Omori K.;  
 RT "the human phosphodiesterase PDE10A gene. Genomic organization and  
 evolutionary relatedness with other PDEs containing GAF domains.";

RL Eur. J. Biochem. 267:5943-5951(2000).  
DR EMBL; AB041779; BAB16368.1; -.  
DR GO; GO:0004112; F:cyclic-nucleotide phosphodiesterase activity; NAS.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 966 MW; FD4B19D5A6C76446 CRC64;

Query Match 25.3%; Score 21; DB 4; Length 8;  
Best Local Similarity 42.9%; Pred. No. 1e+06;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 DPDSFDQ 15  
Db 2 NPQSPFN 8

RESULT 11  
Q9BYF9 PRELIMINARY; PRT; 9 AA.  
AC Q9BYF9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytokeratin 19 (Fragment).  
GN K19.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21539745; PubMed=11682035;  
RA Kagaya M., Kaneko S., Ohno H., Inamura K., Kobayashi K.;  
RT "Cloning and characterization of the 5'-flanking region of human  
cytokeratin 19 gene in human cholangiocarcinoma cell line.";  
RL J. Hepatol. 35:504-511(2001).  
DR EMBL; AB045973; BAB40770.1; -.  
DR GO; GO:0005882; C:intermediate filament; IEA.  
KW Keratin.  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1122 MW; 9E9FC41B45AB45A1 CRC64;

Query Match 25.3%; Score 21; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YSYLQ 6  
Db 4 YSYRQ 8

RESULT 12  
P96319 PRELIMINARY; PRT; 11 AA.  
AC P96319;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Coded portion of proteolysis tag (Fragment).  
OS Desulfovibrio desulfuricans.  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobibrionales;  
OC Desulfobibrionaceae; Desulfobivrio.  
OX NCBI\_TaxID=876;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 27774;  
RX MEDLINE=97128184; PubMed=8972778;  
RA Williams K.P., Bartel D.P.;  
RT "Phylogenetic analysis of tRNA secondary structure.";  
RL RNA 2:1306-1310(1996).  
DR EMBL; U68081; AAB48023.1; -.  
FT NON TER 1  
SQ SEQUENCE 11 AA; 1250 MW; 8576D58CB5ABB5A CRC64;

Query Match 25.3%; Score 21; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSY 4  
Db 6 DYAY 9

RESULT 13  
Q9TQY4 PRELIMINARY; PRT; 12 AA.  
AC Q9TQY4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Glycoprotein H-B N-TERMINAL, GPH-B N-TERMINAL=KEX2/subtilisin-related  
protease (Fragment).  
DE Bos taurus (Bovine).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91340701; PubMed=1874725;  
RA Christie D.L., Batchelor D.C., Palmer D.J.;  
RT "Identification of kex2-related proteases in chromaffin granules by  
partial amino acid sequence analysis.";  
RL J. Biol. Chem. 266:15679-15683(1991).  
FT NON TER 1  
FT NON TER 12  
SQ SEQUENCE 12 AA; 1303 MW; 9F2FF9E2782DC5BA CRC64;

Query Match 25.3%; Score 21; DB 6; Length 12;  
Best Local Similarity 54.5%; Pred. No. 5.9e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 SYLQSDPDPSF 13  
Db 1 SYLXDSALDLP 11

RESULT 14  
Q9R7D6 PRELIMINARY; PRT; 13 AA.  
AC Q9R7D6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 33kD hemagglutinin (Fragment).  
GN HEM33/B.  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Lananna;  
RA Yang G.H.;  
RT "Nontoxic components of Clostridium botulinum type B progenitor  
toxin.";  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U63808; AAB64348.1; -.  
FT NON TER 13  
SQ SEQUENCE 13 AA; 1552 MW; 98356108FAGFD041 CRC64;

Query Match 25.3%; Score 21; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 6.5e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YSYLQDS 8  
Db 1 YSYLQDS 8

Db 4 YSTIONS 10

```
RESULT 15
Q9IBN1
ID Q9IBN1 PRELIMINARY; PRT; 13 AA.
AC Q9IBN1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Influenza A/mayo clinic/103/74 (H1n1), non-structural protein (Seg 8),
DE cooh terminus of ns1 (Fragment).
OS Influenza A virus (strain A/Mayo clinic/103/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11437;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=a/mayo clinic/103/74;
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza a virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; K00960; AAA43523.2; -.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1673 MW; 51550D3C579F56D7 CRC64;
```

```
Query Match 25.3%; Score 21; DB 12; Length 13;
Best Local Similarity 57.1%; Pred. No. 6.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 DYSYLQD 7
Db 2 DLHYLQN 8
```

Search completed: June 3, 2004, 15:34:43  
Job time : 39 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 17:03:29 ; Search time 53 Seconds  
(without alignments)  
79.966 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DYSLQDSPDSFQD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 447529

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_29Jan04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	15	2 AAW15323	AAW15323 Class II
2	83	100.0	15	2 AAY33169	Aay33169 Human tyr
3	83	100.0	15	2 AAY00711	Aay00711 Tumour an
4	83	100.0	15	2 AAY49659	Aay49659 Tumour an
5	83	100.0	15	2 AAY01749	Aay01749 Exemplary
6	83	100.0	15	3 AAY71516	Aay71516 Human Tyr
7	83	100.0	15	3 AAY90800	Aay90800 Human leu
8	83	100.0	15	3 AAB23672	Aab23672 Cytotoxic
9	83	100.0	15	3 AAY92296	Aay92296 Tyrosinas
10	83	100.0	15	3 AAY56611	Aay56611 Tyrosinas
11	83	100.0	15	3 AAY84292	Aay84292 Tumour as
12	83	100.0	15	3 AAY82975	Aay82975 Tyrosinas
13	83	100.0	15	3 AAB02618	Aab02618 Tumour as
14	83	100.0	15	3 AAB08690	Aab08690 Antigenic
15	83	100.0	15	4 AAE02107	Aae02107 Tyrosinas
16	83	100.0	15	4 AAB31350	Aab31350 Exemplary
17	83	100.0	15	4 AAE06837	Aae06837 Human tyr
18	83	100.0	15	5 AAG79140	Abg79140 Human tyr
19	83	100.0	15	6 ADA19544	Adai19544 Human can
20	79	95.2	15	2 AAW15354	AAW15354 Class II
21	79	95.2	15	2 AAW15331	AAW15331 Class II
22	79	95.2	15	2 AAW15332	AAW15332 Class II
23	77	92.8	14	2 AAW15324	AAW15324 Class II
24	77	92.8	15	2 AAW15353	AAW15353 Class II
25	75	90.4	15	2 AAW15329	AAW15329 Class II

## ALIGNMENTS

### RESULT 1

AAW15323

ID AAW15323 standard; peptide; 15 AA.

AC AAW15323;

DT 09-FEB-1998 (first entry)

DE Class II restricted melanoma tyrosinase derived antigenic peptide 3.

XX Major histocompatibility complex; MHC; Class II; tyrosinase; vaccine;

KW immune response; immunogenic peptide; melanoma; treatment;

KW protective antibody; immune cells; CD8+ T cell; CD4+ T cell.

OS Synthetic.

OS Homo sapiens.

PN WO9711669-A2.

XX WO9711669-A2.

XX 03-APR-1997.

XX 25-SEP-1996; 96WO-US015346.

XX 26-SEP-1995; 95US-00533895.

(USGH ) US DEPT HEALTH & HUMAN SERVICES.

Topalian SL, Rosenberg SA, Robbins PF;

WPI; 1997-212652/19.

Major histocompatibility complex Class H immunogenic peptide - used to prevent or treat melanoma in mammal by stimulating production of protective antibodies or immune cells.

Claim 2; Page 59; 79pp; English.

Peptides AAW15321-56 are major histocompatibility complex (MHC) Class II restricted melanoma peptides, derived from tyrosinase. Tumour reactive human CD4+ and CD8+ T cells recognise melanoma antigens encoded by the tyrosinase gene. The present sequence is derived from amino acids 448-462. The peptides may be used as a vaccine, either prophylactically in advance of any evidence of melanoma, or therapeutically to enhance the patient's own immune response. The immunogenic peptides can be used to prevent or treat melanoma in a mammal by stimulating the production of protective antibodies or immune cells, preferably immune positive CD4+ T cells

SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQD 15  
| | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPDQD 15

RESULT 2

AAV33169  
ID AAY33169 standard; peptide; 15 AA.

XX AC AAY33169;

XX DT 17-NOV-1999 (first entry)

XX DE Human tyrosinase peptide #8.

XX KW Human; protein delivery; Yersinia sp; effector gene; mutant; antigen;  
XX KW immune response; cytotoxic T-lymphocyte; CTL; vaccination; treatment;  
XX KW pathological disorder; tyrosinase.

XX OS Homo sapiens.

XX PN WO9945098-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-IB000587.

XX PR 06-MAR-1998; 98US-00036582.

XX PA (VBRU/) VAN DER BRUGGEN P B.  
XX PA (CORN/) CORNELIS G R.

XX PA (BOLA/) BOLLAND A M.

XX PA (BOON/) BOON-FALLEUR T R.

XX PI Van Der Bruggen PB, Cornelis GR, Bolland AM, Boon-Falleur TR;  
XX PS WPI; 1999-540840/45.

XX DR 1999-540840/45.

XX PT New mutant Yersinia strains useful for treating a pathological disorder.  
XX PS Example 1; Page 70; 80pp; English.

XX CC This invention describes a novel mutant Yersinia (Y1) strain, comprising  
XX CC mutation(s) in effector-encoding gene(s) and deficient in the production  
XX CC of functional effector protein(s). The invention describes (1) a  
XX CC quintuple mutant Yersinia strain, having the designation Yersinia  
XX CC enterocolitica YOPHOMP or Yersinia pseudotuberculosis YOPHMOV; (2) an  
XX CC expression vector (EV1) for delivering a heterologous protein into a  
XX CC eukaryotic cell, comprising in the 5'3' direction; (3) a Yersinia or  
XX CC mutant Yersinia strain for delivering a heterologous protein into a  
XX CC eukaryotic cell, comprising contacting the cell with a Y1 transformed  
XX CC cell with the above vector (Y1-EV1); (4) a method for delivering a  
XX CC heterologous protein into a eukaryotic cell, comprising contacting the  
XX CC cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method  
XX CC for inducing an immune response specific for a heterologous protein; (6)  
XX CC a method for inducing a cytotoxic T-lymphocyte (CTL) response specific  
XX CC for a heterologous protein; (7) a method for determining the efficacy of  
XX CC an antigen vaccination regimen in a subject. Y1 is used to treat a  
XX CC pathological disorder, by providing recombinant Yersinia for the safe  
XX CC delivery of proteins into eukaryotic cells. AAY33147-V33178 are human-  
XX CC derived peptides used to illustrate the method of the invention

SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQD 15  
| | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPDQD 15

RESULT 3

AAV00711  
ID AAY00711 standard; peptide; 15 AA.

XX AC AAY00711;

XX DT 12-MAY-1999 (first entry)

XX DE Tumour antigen booster peptide Tyrosinase HLA-DR4.

XX KW Tumour antigen; booster peptide; immune response modulation; allergy;  
XX KW immune response enhancer; tumour cell; tumour rejection antigen;  
XX KW leukocyte antigen-presenting molecule; autoimmune disease;  
XX KW allograft rejection.

XX OS Homo sapiens.

XX PN WO9858956-A2.

XX PD 30-DEC-1998.

XX PF 19-JUN-1998; 98WO-US012894.

XX PR 23-JUN-1997; 97US-00880979.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Warnier G, Uyttenhove C, Boon-Falleur T;  
XX PS WPI; 1999-105612/09.

XX DR 1999-105612/09.

XX PT Immunization methods using viruses expressing antigen for priming and  
XX PT booster immunizations - useful for modulating immune responses against  
XX PT antigen, e.g. enhancing immune response against tumour cells expressing  
XX PT tumour rejection antigens.

XX PS Disclosure; Page 9; 33pp; English.

XX CC This sequence represents a tumour antigen booster peptide that can be  
XX CC used in the method of the invention. The method is for for modulating an  
XX CC immune response in a mammal against an antigen, and comprises: (A)  
XX CC inducing an immune response by: (i) administering a virus containing a  
XX CC nucleic acid molecule encoding the antigen or its precursor to generate  
XX CC an immune response; and (ii) administering at least one booster dose  
XX CC comprising a peptide including the antigen, in an adjuvant, in a combined  
XX CC amount effective to enhance the initial immune response; or (B) reducing  
XX CC an immune response as defined for (A) but using a non-adjuvant with the  
XX CC peptide which includes the antigen, in an amount effective to reduce the  
XX CC initial immune response. Method (A) is used to enhance the immune  
XX CC response against tumour cells expressing tumour rejection antigens, and  
XX CC against pathogens in subjects having human leukocyte antigen-presenting  
XX CC molecules. Method (B) is used to reduce the immune response in allergy,  
XX CC autoimmune disease, and allograft rejection. Method (A) provides an  
XX CC immunisation method which, unlike prior art, is not limited by the host  
XX CC immune response against viral vectors

SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPDQD 15  
| | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPDQD 15

## RESULT 4

RAY49659  
ID AAY49659 standard; peptide; 15 AA.

XX AC AAY49659;  
XX AC AAY49659;

DT 14-JAN-2000 (first entry)

DE Tumour antigenic peptide SEQ ID NO:26.

XX Human; sdph3.10; SAGE; sdp3.8; HAGE; sdp3.5; TRAP; sarcoma;  
KW tumour rejection antigen precursor; tumour associated nucleic acid;  
KW carcinoma; cancer; immune response; diagnosis.

XX OS Synthetic.

XX PN WO9953061-A2.

XX PD 21-OCT-1999.

XX PF 14-APR-1999; 99WO-US008163.

XX PR 15-APR-1998; 98US-00060706.

XX PR 27-JUL-1998; 98US-00122989.

XX PR 30-OCT-1998; 98US-00183706.

XX PR 30-OCT-1998; 98US-00183789.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Martelange V, De Smet C, Boon-Falleur T;

XX DR WPI; 1999-620430/53.

XX PT New nucleic acid encoding sarcoma-associated gene products, useful for  
XX diagnosing, e.g. treating and preventing cancer.

XX PS Disclosure; Page 25; 93pp; English.

XX The present invention describes sarcoma-associated gene products (I).  
CC Agents, specifically sarcoma associated nucleic acids (II) or their  
CC expression products that are tumour rejection antigens (TRA), that  
CC selectively increase formation of HLA (human leucocyte antigen)/(I)  
CC complexes are used for treating cancer, especially sarcoma and carcinoma,  
CC in humans and other animals. Compositions containing autologous cytolytic  
CC T cells (CTL), specific for the HLA/(I) complex, are similarly useful,  
CC also transformed cells that stimulate such CTL in vivo. (II) are also  
CC used: (i) as source of therapeutic antisense sequences that reduce  
CC expression of (II); (ii) for recombinant production of (I); (iii)  
CC particularly its fragments, as primers and probes in usual hybridisation  
CC and amplification assays, for diagnosis, prognosis and monitoring of  
CC tumours, or for measuring binding specificity of HLA molecules or CTL  
CC clones; (iv) to identify related sequences; and (v) for generating  
CC transgenic animals, e.g. for studying cancer and immune responses to it.  
CC (I) are used to raise specific antibodies (Ab) and therapeutically Ab  
CC are used to diagnose tumours in immunoassays, also for delivering drugs,  
CC toxins, imaging agents etc. to (I)-expressing cells. AAY49637 to AAY49670  
CC represent exemplary tumour antigenic peptides given in the present  
CC invention

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15

Db 1 DYSYLQSDPDPSFQD 15

## RESULT 5

AAY01749

ID AAY01749 standard; peptide; 15 AA.

XX AC AAY01749;  
XX AC AAY01749;

DT 25-JUN-1999 (first entry)

DE Exemplary antigenic peptide derived from Tyrosinase.

XX MAG-3; tumour associated gene; human leucocyte antigen Class II;  
KW autologous CD4+ cell; MAG-3 related disease; cancer; melanoma;  
KW osteosarcoma; leukemia; carcinoma.

XX OS Homo sapiens.

XX PN WO9914326-A1.

XX PD 25-MAR-1999.

XX PF 04-SEP-1998; 98WO-US018601.

XX PR 12-SEP-1997; 97US-00928615.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PA (UVVR-) UNIV VRIJE BRUSSEL.

XX PI Thielemans K, Heirman C, Corthals J, Chaux P, Stroobant V;

XX PI Boon-Falleur T, Van Der Bruggen P, Luiten R;

XX DR WPI; 1999-244031/20.

XX PT Isolated peptides that bind to human leucocyte antigen class II  
XX molecules.

XX PS Disclosure; Page 29; 88pp; English.

XX The present sequence represents an exemplary tumour associated peptide  
CC antigen. The specification describes a MAG-3 tumour associated gene.  
CC Peptides (AAY01721-25) that bind human leucocyte antigen (HLA) Class II  
CC molecules can be derived from the MAG-3 protein. These peptides and  
CC autologous CD4+ cells that bind to a complex of MAG-3 peptide and HLA  
CC Class II, are used to treat MAG-3 related diseases, particularly cancers  
CC (e.g. melanoma, osteosarcoma, leukemia and various forms of carcinoma).  
CC The peptides are also used to produce specific antibodies. Detection of  
CC of the peptides, e.g. in binding assays, particularly with antibodies, is  
CC used for diagnosis of such diseases

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15

Db 1 DYSYLQSDPDPSFQD 15

## RESULT 6

AAY71516

ID AAY71516 standard; peptide; 15 AA.

XX AC AAY71516;

XX DT 12-OCT-2000 (first entry)

XX DE Human Tyrosinase peptide-6.

XX Tyrosinase; human; Tumour Rejection Antigen; TRA; tumour; cancer; HLA;

XX KW Human Leucocyte Antigen; MHC; Major Histocompatibility Complex; CTL;  
XX cytolytic T-lymphocyte; immune response stimulator; prophylaxis; therapy;  
XX diagnosis; TNF; tumour necrosis factor; vaccine; cytostatic.

XX OS Homo sapiens.

XX OS



PN WO2000032769-A2.  
 XX 08-JUN-2000.  
 XX 26-NOV-1999; 99WO-IB002018.  
 XX 27-NOV-1998; 98GB-00026143.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;  
 PI WPI; 2000-412317/35.  
 XX Novel polypeptides expressed in tumor cells useful for treating cancers  
 PT have an ability to complex with a major histocompatibility complex  
 PT molecule and comprises a specific unbroken amino acid sequence.  
 XX  
 PS Disclosure; Page 19; 80pp; English.  
 XX  
 CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and  
 CC decapeptide sequences, that function as tumour rejection antigens (TRAs).  
 CC These peptides are capable of forming a complex with major  
 CC histocompatibility complex (MHC) molecule type HLA-A2:1 (Human Leucocyte  
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune  
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune  
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,  
 CC therapy and diagnosis of tumours and are effective in controlling or  
 CC preventing tumour growth. The present sequence is the human Tyrosinase  
 CC peptide-6, that corresponds to residues 448-462 of the tumour associated  
 CC gene, tyrosinase encoding protein. It can be administered to induce or  
 CC enhance an immune response and is presented by HLA-DR4 complex. This  
 CC peptide can serve as a tumour rejection antigen (TRA) and in combination  
 CC with adjuvants, can produce vaccines useful for treating a variety of  
 CC tumours  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDSPDSFQD 15  
 Db |||||  
 1 DYSYLQSDSPDSFQD 15  
 RESULT 7  
 AAY90800  
 ID AAY90800 standard; peptide; 15 AA.  
 XX  
 AC AAY90800;  
 XX  
 DT 25-AUG-2000 (first entry)  
 XX  
 DE Human leukocyte antigen DR4 peptide SEQ ID NO:29.  
 XX  
 KW Human leukocyte antigen; HLA-B35; binding; recognition; lysis;  
 KW cytolytic T cell; tyrosinase; immune response; diagnosis; identification;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200021551-A1.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 04-OCT-1999; 99WO-US023038.  
 XX  
 PR 09-OCT-1998; 98US-00169717.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX

PI Ooms A, De Giovanni G, Morel S, Van Den Eynde B, Boon-Falleur T;  
 XX WPI; 2000-317842/27.  
 XX  
 CC Isolated peptides, sometimes derived from tyrosinase, which bind to HLA-  
 CC B35 leading to recognition and lysis of the resulting complexes by  
 CC cytolytic T cells.  
 XX  
 PS Example 3; Page 9; 20pp; English.  
 XX  
 CC The present invention describes isolated peptides which bind to human  
 CC leukocyte antigen (HLA)-B35 molecules leading to recognition and lysis of  
 CC the resulting complexes by cytolytic T cells. The isolated peptides are  
 CC sometimes derived from tyrosinase. Compositions comprising the peptides  
 CC of the invention can be used to generate immune responses, preferably in  
 CC humans, but also in non-human animals to generated immune components  
 CC which can then be used to treat humans or diagnostically.  
 CC Therapeutically, the peptides are useful in generation of cytolytic T  
 CC cells either in vitro or in vivo which specifically lyse pathogenic  
 CC cells. The peptides can also be used to identify HLA-B35 positive cells,  
 CC or to remove HLA-B35 positive cells from mixtures containing such cells.  
 CC Nucleic acid molecules encoding the peptides can be used inter alia as  
 CC probes to identify cells which are expressing tyrosinase. The present  
 CC sequence represents an HLA binding peptide used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDSPDSFQD 15  
 Db |||||  
 1 DYSYLQSDSPDSFQD 15  
 RESULT 8  
 AAB23672  
 ID AAB23672 standard; peptide; 15 AA.  
 XX  
 AC AAB23672;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:24.  
 XX  
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytostatic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200049041-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-JP000941.  
 XX  
 PR 19-FEB-1999; 99JP-00041535.  
 XX  
 PA (SUME ) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Udono H, Yui K;  
 XX WPI; 2000-543748/49.  
 XX  
 CC Fused protein capable of inducing cellular immune response, useful as  
 CC active ingredient for drug compositions in preventing and/or treating  
 CC infectious diseases such as malaria or cancer.  
 XX  
 PS Claim 7; Page 57; 72pp; Japanese.

XX The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (I) has cytostatic, immunostimulant and  
 CC protooncogene activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed CTL epitope for  
 CC use in a fused protein of the present invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDSFQD 15  
 Db 1 DYSYLQSDPDSFQD 15  
 RESULT 9  
 AAY92296  
 ID AAY92296 standard; peptide; 15 AA.  
 AC AAY92296;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Tyrosinase antigenic peptide epitope (residues 448-462).  
 KW Tyrosinase; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;  
 KW human leukocyte antigen; HLA.  
 XX Homo sapiens.  
 OS  
 XX WO200020445-A2.  
 PN 13-APR-2000.  
 PD  
 XX 15-SEP-1999; 99WO-IB001664.  
 XX  
 PF 02-OCT-1998; 98US-00165863.  
 PR 09-APR-1999; 99US-00289350.  
 XX  
 PA (CHAU//) CHAUX P.  
 PA (LUIT//) LUITEN R.  
 PA (DEMO//) DEMOTTE N.  
 PA (DUFF//) DUFFOUR M.  
 PA (LURQ//) LURQUIN C.  
 PA (TRAV//) TRAVESARI C.  
 PA (STRO//) STROBANT V.  
 PA (CORN//) CORNELIS G R.  
 PA (BOON//) BOON-FALLEUR T.  
 PA (VBRU//) VAN DER BRUGEN P.  
 PA (SCHU//) SCHULTZ E.  
 PA (WARN//) WARNIER G.  
 XX  
 PI Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;  
 PI Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;  
 PI Schultz E, Warnier G;  
 XX  
 DR WPI; 2000-303739/26.  
 XX  
 PT Isolation of cytotoxic T-lymphocytes clones by successive steps of  
 PT stimulation and testing of lymphocytes with antigen presenting cells  
 PT which present antigens derived from different expression systems.  
 XX

PS Disclosure; Page 22; 99pp; English.  
 XX  
 CC A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones  
 CC comprises successive steps of stimulation and testing of lymphocytes with  
 CC antigen presenting cells (APCs) which present antigens derived from  
 CC different expression systems. The CTL clones isolated recognize specific  
 CC antigenic peptides of proteins, preferably of the MAGE family. The APC is  
 CC autologous and each expression systems is different from at least one of  
 CC the other expression systems, therefore isolating a cytotoxic T cell  
 CC clone specific for the protein. The method can also be used to identify  
 CC an antigenic peptide epitope. Isolated CTL clones specific for a  
 CC peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells  
 CC specific for the complexes, peptides or cells which present the complexes  
 CC on the cell surface are useful for treating pathological conditions  
 CC characterized by abnormal expression of the complexes  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDPDSFQD 15  
 Db 1 DYSYLQSDPDSFQD 15  
 RESULT 10  
 AAY56611  
 ID AAY56611 standard; peptide; 15 AA.  
 AC AAY56611;  
 XX  
 DT 21-FEB-2000 (first entry)  
 XX  
 DE Tyrosinase gene MHC molecule HLA-DR4 peptide SEQ ID NO:27.  
 KW HLA-A\*0201; human leukocyte antigen; cytolytic T cell; CTL; tumour;  
 KW Melan-A; peripheral blood lymphocyte; PBL; immune complex; melanoma;  
 KW MHC molecule; beta2-microglobulin; cytotoxic T lymphocyte; vaccine;  
 KW immune response; cancer; tyrosinase; tumour rejection antigen;  
 KW major histocompatibility complex.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9950637-A2.  
 PN 07-OCT-1999.  
 PD  
 XX 25-MAR-1999; 99WO-US006615.  
 XX  
 PR 27-MAR-1998; 98US-00049850.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (UYOX-) UNIV OXFORD.  
 XX  
 PI Romero P, Dunbar R, Valmori D, Ogg G, Cerrotini J, Cerundolo V;  
 PI Pittet M;  
 XX  
 DR WPI; 2000-052636/04.  
 XX  
 PT New isolated complex of binding partners and immune complexes containing  
 PT major histocompatibility molecules and peptide, used to isolate and detect  
 PT cytotoxic T cells, particularly directed against cancer.  
 XX  
 PS Example 50; Page 64; 91pp; English.  
 XX  
 CC The present invention describes an isolated complex (A) comprising: (i)  
 CC first and second binding partners (Bp1, Bp2); and (ii) several immune  
 CC complexes (IC) containing a major histocompatibility complex (MHC)  
 CC molecule (I), a beta2-microglobulin molecule (b2MG) and a peptide (II)  
 CC that binds specifically to (I). (A) are used for analysis of cytolytic T

CC cells (CTL) for characterisation of an immune response to tumours or for  
 CC monitoring vaccine trials. Particularly they are used to isolate or  
 CC detect particular CTL (especially those in tumour-infiltrated lymph  
 CC nodes), including visualisation of antigen-specific CTL and determination  
 CC if the cells have been activated by in vivo exposure to antigen. Isolated  
 CC precursor cells may be expanded in vitro to produce cells with high  
 CC tumoricidal activity, for therapeutic or diagnostic use. A method for use  
 CC the present invention allows: (i) preselection of T cell clones for use  
 CC in immunotherapy according to their homing molecules; and (ii) improves  
 CC the lytic activity of T cells populations by inhibition of natural killer  
 CC cell receptors. The present sequence represents a peptide used in the  
 CC exemplification of the present invention

XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQSDSDPSFQD 15  
 Db 1 DYSYLQSDSDPSFQD 15  
 |||||

RESULT 11  
 AAY84292  
 ID AAY84292 standard; peptide; 15 AA.

XX AC AAY84292;  
 XX DT 12-JUL-2000 (first entry)  
 XX DE Tumour associated antigen derived from tyrosinase.  
 XX KW tumour rejection antigen; macrophage colony stimulating gene;  
 XX KW macrophage-colony stimulating factor; antigen presenting cell;  
 XX KW human leukocyte antigen; CD8+ cytotoxic T lymphocyte.

XX OS Homo sapiens.  
 XX PN WO200013699-A1.  
 XX PD 16-MAR-2000.

XX PF 03-SEP-1999; 99WO-US020344.  
 XX PR 04-SEP-1998; 98US-0099077P.  
 XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Probst-Kepper M, Van Den Eynde B, Boon-Falleur T;  
 XX DR WPI; 2000-256859/22.

XX PT Isolated polypeptide used to treat subjects having a disorder  
 PT characterized by expression of alternative open reading frame macrophage-  
 PT colony stimulating factor comprises 25 amino acid residue sequence.

XX PS Disclosure; Page 21; 74pp; English.

XX CC AAY84270-Y84303 represent peptides which are tumour associated antigens.  
 CC They can be administered in conjunction with the tumour rejection antigen  
 CC precursor of the invention to induce anti-tumour responses. The tumour  
 CC rejection antigen precursor of the invention is encoded by an alternative  
 CC open reading frame (ORF) of human macrophage colony stimulating gene.  
 CC Peptides derived from the alternative ORF of macrophage-colony  
 CC stimulating factor, when presented by an antigen presenting cell having a  
 CC human leukocyte antigen (HLA) class I molecule, effectively induce the  
 CC activation and proliferation of CD8+ cytotoxic T lymphocytes. Polypeptide  
 CC and nucleic acids derived from the alternate ORF of macrophage-colony  
 CC stimulating factor are useful for enriching selectively a population of T  
 CC lymphocytes with CD8+ T lymphocytes. They are also useful for diagnosing  
 CC a disorder characterized by expression of the polypeptide, and for

CC identifying functional variants and mimetics  
 XX Sequence 15 AA;  
 SQ

Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDSDPSFQD 15  
 Db 1 DYSYLQSDSDPSFQD 15  
 |||||

RESULT 12  
 AAY82975  
 ID AAY82975 standard; peptide; 15 AA.

XX AC AAY82975;  
 XX DT 19-JUN-2000 (first entry)  
 XX DE Tyrosinase tumour associated antigen.

XX KW Tumour; tumour associated antigen; retrovirus; antisense; treatment;  
 KW probe; primer; HLA; cytotoxic T-lymphocyte; cancer; testis; antibody;  
 KW CTL; helper T-lymphocyte; MAGE; BAGE; RAGE; Gnt-V; MDM; CDK4;  
 KW beta catenin; tyrosinase; Melan-A; gp100; PRAME.

XX OS Homo sapiens.  
 XX PN WO200006598-A1.

XX PD 10-FEB-2000.  
 XX PF 15-JUL-1999; 99WO-US016236.  
 XX PR 29-JUL-1998; 98US-00124398.

XX PA (LUDW-) LUDWIG INST CANCER RES.  
 XX PI Coulie P, Boon-Falleur T;  
 XX DR WPI; 2000-205453/18.

XX PT Novel nucleic acids encoding melanoma associated gene products and their  
 PT fragments and variants, useful for treating endogenous retrovirus  
 PT mediated tumors, especially melanomas.

XX PS Disclosure; Page 26; 77pp; English.

XX CC Tumor associated disorders (e.g. endogenous retrovirus mediated tumors,  
 CC especially melanomas) can be treated or ameliorated by administering  
 CC antisense nucleic acid to reduce the expression of tumour associated  
 CC genes such as HERV-AVL3-B. Progression of a disorder characterized by the  
 CC expression of the HERV-AVL3-B endogenous retrovirus tumor rejection  
 CC antigen (ERTRA) can be diagnosed or monitored by contacting a non-testis  
 CC biological sample with an agent that binds to the complex and determining  
 CC the interaction. A disorder can also be treated by administering an agent  
 CC that enriches the presence of HLA and HERV-AVL3-B ERTRA or by  
 CC administering autologous cytotoxic T-cells sufficient to ameliorate the  
 CC disorder. Fragments of the HERV-AVL3-B coding sequence are useful as  
 CC probes or amplification primers for determining the expression of HERV-  
 CC AVL3-B genes, to express tumor associated polypeptides in vivo and in  
 CC vitro and to prepare fragments of such polypeptides to synthesize  
 CC antibodies. Antigenic peptides of HERV-AVL3-B can be useful for  
 CC generating antibodies either alone or as fusion proteins, as components  
 CC of immunoassay and for determining the binding specificity of HLA  
 CC molecules and/or cytotoxic T lymphocyte (CTL) for HERV-AVL3-B proteins.  
 CC Peptides derived from the HERV-AVL3-B coding sequence and which are  
 CC presented by MHC molecules and recognised by CTL or helper T-lymphocytes  
 CC can be combined with peptides from other tumour rejection antigens by  
 CC preparation of hybrid nucleic acids or polypeptides to produce polypeptides.  
 CC This exemplary tumour associated peptide antigen corresponds to amino

CC acids 448-462 of the tyrosinase polypeptide. See also AAY82953-Y82986

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15

Db 1 DYSYLQSDPDPSFQD 15

RESULT 13

AAAB02618  
 ID AAB02618 standard; peptide; 15 AA.

XX AC AAB02618;

DT 18-AUG-2000 (first entry)

DE Tumour associated peptide antigen from Tyrosinase #7.

KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;  
 KW cancer; human; tumour; tumour associated gene product.

XX OS Homo sapiens.

PN WO200020581-A1.

XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-US021230.

XX PR 05-OCT-1998; 98US-00166448.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PA (UYVR-) UNIV VRIJE BRUSSEL.

XX PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;

XX PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;

XX PI Heirman C;

XX DR WPI; 2000-317713/27.

XX PT New MAGE-A3 class II binding peptides, useful to diagnose and treat  
 PT tumors, are fragments of MAGE-A3 which bind to and are presented to T  
 PT lymphocytes by human leukocyte antigen class II molecules.

XX PS Disclosure; Page 33; 119pp; English.

XX CC The present invention relates to MAGE-A3 (tumour associated gene product)  
 CC human leukocyte antigen (HLA) class II-binding peptides (see AAB02566-  
 CC B02595, and AAB02633-B02637). These peptides are presented to T cells in  
 CC the context of HLA class II molecules. The peptides stimulate the  
 CC activity and proliferation of CD4+ T lymphocytes. The invention also  
 CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928 and  
 CC AAA37938-A37940). The peptides and nucleotide sequences can be used to  
 CC create antibodies against the MAGE-A3 peptides, the antibodies, peptides  
 CC and nucleotide sequences can be used to create a vaccine. The peptides  
 CC are used to diagnose or treat a disorder characterized by expression of  
 CC MAGE-3, particularly cancer. The methods can also be used in the  
 CC diagnosis of disorders associated with MAGE-3 expression. Included in the  
 CC invention are other human tumour antigens (see AAB02596-B02637), and PCR  
 CC primers used in the course of the invention (see AAA37929-A37937 and  
 CC AAA37941-A37942)

XX SQ Sequence 15 AA;

Query Match

Best Local Similarity 100.0%; Score 83; DB 3; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15

Db 1 DYSYLQSDPDPSFQD 15

RESULT 14

AAAB08690  
 ID AAB08690 standard; peptide; 15 AA.

XX AC AAB08690;

DT 02-JAN-2001 (first entry)

DE Antigenic peptide from tumour rejection antigen tyrosinase.

KW Epha3; HLA class II-binding peptide; human leukocyte antigen; antigen;  
 KW CD4+ T lymphocyte; tumour associated gene; vaccine.

XX OS Homo sapiens.

PN WO200050589-A1.

XX PD 31-AUG-2000.

XX PF 18-FEB-2000; 2000WO-US004326.

XX PR 22-FEB-1999; 99US-0121170P.

XX PR 08-OCT-1999; 99US-0158566P.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chiari R, Coulie P, Boon-Falleur T;

XX PI WPI; 2000-572089/53.

XX PT Novel tyrosine kinase receptor, Epha3 human leukocyte antigen (HLA) class  
 PT II binding peptide and nucleic acid encoding the receptor, useful for  
 PT diagnosing and treating conditions characterized by expression of Epha3  
 PT gene.

XX PS Disclosure; Page 35; 107pp; English.

XX CC AAB08668-B08704 represent antigenic peptides characteristic of tumours.  
 CC The peptides may be combined in vaccines with a human Epha3 HLA (human  
 CC leukocyte antigen) class II-binding peptide. Epha3 antigens, when  
 CC presented by an antigen presenting cell having a HLA class II molecule,  
 CC effectively induce activation and proliferation of CD4+ T lymphocytes.  
 CC Epha3 is a tumour associated gene. Epha3 HLA binding peptides are used  
 CC for selectively enriching a population of T lymphocytes. The peptides are  
 CC also used for diagnosing a disorder characterized by Epha3 or Epha3 HLA  
 CC binding peptide expression. The peptides are also used to treat a  
 CC disorder characterized by Epha3 expression. The Epha3 binding peptides  
 CC are useful in producing vaccines and antibody

XX SQ Sequence 15 AA;

Query Match

Best Local Similarity 100.0%; Score 83; DB 3; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDPSFQD 15

Db 1 DYSYLQSDPDPSFQD 15

RESULT 15

AAE02107  
 ID AAE02107 standard; peptide; 15 AA.

XX AC AAE02107;

XX DT 31-JUL-2001 (first entry)

XX

DE Tyrosinase human leukocyte antigen-DR4-binding peptide #2.  
XX Human; cytostatic; immunogen; Tyrosinase; human leukocyte antigen; HLA;  
KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;  
KW brain tumour; sarcoma; vaccine; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200129220-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 19-OCT-2000; 2000WO-US028852.  
XX  
PR 19-OCT-1999; 99US-0160374P.  
PR 01-FEB-2000; 2000US-0179570P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;  
XX WPI; 2001-328498/34.  
XX  
PT New antigenic peptides derived from MAGE-A12 polypeptides, useful for  
PT diagnosis and treatment of cancer, such as bladder, lung, breast, brain,  
PT prostate and renal carcinomas.  
XX  
PS Disclosure; Page 20; 69pp; English.  
XX  
CC The patent discloses antigenic peptides derived from MAGE-A12 protein and  
CC presented by human leukocyte antigens (HLAs). These antigenic peptides  
CC when presented by an antigen presenting cell having a HLA class I  
CC molecule, effectively induce the activation and proliferation of CD8+  
CC cytotoxic T lymphocytes (CTLs). MAGE-A12 is useful for treating a subject  
CC having a disorder characterised by expression of MAGE-A12. The protein  
CC microarray comprising MAGE-A12 is useful for diagnosing a disorder,  
CC especially cancer, by determining the binding of an antibody, T  
CC lymphocytes or a HLA molecule isolated from the subject suspected of  
CC having the disorder characterised by the expression of MAGE-A12. MAGE-A12  
CC is useful for treating cancers, including bladder carcinomas, melanomas,  
CC oesophageal, lung, head and neck, breast, colorectal carcinomas, and to  
CC myelomas, brain tumours, sarcomas, prostate and renal carcinomas, and to  
CC produce antibodies. MAGE-A12 antibodies are useful for diagnosing  
CC disorders characterised by expression of MAGE-A12 immunogenic  
CC polypeptide. These MAGE-A12 peptides are used as vaccines. They are also  
CC used in gene therapy. The present sequence is an antigenic peptide  
CC derived from Tyrosinase. This peptide which is characteristic of tumours  
CC is presented by HLA-DR4 MHC (major histocompatibility complex) and is  
CC recognised by CTLs  
XX  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYSYLQSDPDSFQD 15  
DB 1 DYSYLQSDPDSFQD 15  
RESULT 16  
AAB31350  
ID AAB31350 standard; peptide; 15 AA.  
XX  
AC AAB31350;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Exemplary antigen characteristic of tumours, derived from tyrosinase.  
XX MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;  
KW MAGE-A1 HLA class II-binding protein; vaccine.  
XX  
DE Tyrosinase human leukocyte antigen-DR4-binding peptide #2.  
XX Human; cytostatic; immunogen; Tyrosinase; human leukocyte antigen; HLA;  
KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;  
KW brain tumour; sarcoma; vaccine; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200129220-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 19-OCT-2000; 2000WO-US028852.  
XX  
PR 19-OCT-1999; 99US-0160374P.  
PR 01-FEB-2000; 2000US-0179570P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;  
XX WPI; 2001-328498/34.  
XX  
PT New antigenic peptides derived from MAGE-A12 polypeptides, useful for  
PT diagnosis and treatment of cancer, such as bladder, lung, breast, brain,  
PT prostate and renal carcinomas.  
XX  
PS Disclosure; Page 20; 69pp; English.  
XX  
CC The patent discloses antigenic peptides derived from MAGE-A12 protein and  
CC presented by human leukocyte antigens (HLAs). These antigenic peptides  
CC when presented by an antigen presenting cell having a HLA class I  
CC molecule, effectively induce the activation and proliferation of CD8+  
CC cytotoxic T lymphocytes (CTLs). MAGE-A12 is useful for treating a subject  
CC having a disorder characterised by expression of MAGE-A12. The protein  
CC microarray comprising MAGE-A12 is useful for diagnosing a disorder,  
CC especially cancer, by determining the binding of an antibody, T  
CC lymphocytes or a HLA molecule isolated from the subject suspected of  
CC having the disorder characterised by the expression of MAGE-A12. MAGE-A12  
CC is useful for treating cancers, including bladder carcinomas, melanomas,  
CC oesophageal, lung, head and neck, breast, colorectal carcinomas, and to  
CC myelomas, brain tumours, sarcomas, prostate and renal carcinomas, and to  
CC produce antibodies. MAGE-A12 antibodies are useful for diagnosing  
CC disorders characterised by expression of MAGE-A12 immunogenic  
CC polypeptide. These MAGE-A12 peptides are used as vaccines. They are also  
CC used in gene therapy. The present sequence is an antigenic peptide  
CC derived from Tyrosinase. This peptide which is characteristic of tumours  
CC is presented by HLA-DR4 MHC (major histocompatibility complex) and is  
CC recognised by CTLs  
XX  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYSYLQSDPDSFQD 15  
DB 1 DYSYLQSDPDSFQD 15  
RESULT 17  
AAB06837  
ID AAB06837 standard; peptide; 15 AA.  
XX  
AC AAB06837;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human tyrosinase antigenic peptide #7.  
XX  
KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;  
KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;  
KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;  
KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;  
KW gene therapy; tumour rejection antigen; TRA; human; tyrosinase; MHC;  
KW major histocompatibility complex.  
XX  
OS Homo sapiens.  
XX  
PN WO200153833-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 19-JAN-2001; 2001WO-US002008.  
XX  
PR 20-JAN-2000; 2000US-0177242P.

25-OCT-2000; 2000US-0243212P.  
(LUDW-) LUDWIG INST CANCER RES.  
Luiten R, Boon-Palleur T, Van Der Bruggen P, Stroobant V;  
Demotte N, Schultz E;  
WPI; 2001-488724/53.  
Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used in diagnosis and treatment of a disorder characterized by expression of MAGE-A1 or -A3.  
Disclosure; Page 28; 103pp; English.  
The invention relates to functional variants and isolated mimetics of a MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described in the specification. MAGE genes encode tumour rejection antigens (TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules. The MAGE antigenic peptide acts by binding to HLA molecules on tumour cells and stimulating recognition of these cells and thus signalling them to the immune system for destruction. The peptide when presented by HLA molecule induces the activation and stimulation of CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to treat and diagnose disorders characterised by expression of MAGE-A1 or -A3. Disorders include cancers e.g. melanomas, oesophageal, lung, head and neck, breast, colorectal, prostate, renal, bladder, hepatocellular, papillary thyroid and gastric carcinomas, myelomas, brain tumours, sarcomas, seminomas, and ovarian tumours. The present sequence is human tyrosinase tumour associated antigenic peptide presented by major histocompatibility complex (MHC) HLA -DR4. The antigenic peptide is used in combination with peptides of the invention for inducing an immune response  
Sequence 15 AA;  
Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DYSYLQSDPDSFQD 15  
Db 1 DYSYLQSDPDSFQD 15  
RESULT 18  
ABG79140  
ID ABG79140 standard; peptide; 15 AA.  
AC ABG79140;  
DT 15-NOV-2002 (first entry)  
DE Human tyrosinase class II HLA tumour-restricted antigen peptide #2.  
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen; lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia; Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer; kidney cancer; adenocarcinoma; breast cancer; prostate cancer; ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell; tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA; cytostatic; human.  
OS Homo sapiens.  
XX WO200264057-A2.  
XX 22-AUG-2002.  
XX 15-FEB-2002; 2002WO-US005212.  
XX 15-FEB-2001; 2001US-0268687P.

(BAYU ) BAYLOR COLLEGE MEDICINE.  
Wang R;  
WPI; 2002-627577/67.  
Novel composition for treating a disease in an animal, comprises an immune effector cell and cell penetrating peptide associated with an antigen or antibody.  
Disclosure; Page 22; 61pp; English.  
The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (1) a vaccine comprising (I); CPP associated with an antigen, and a pharmaceutically acceptable carrier and (2) preparing a composition for a disease, by providing (I) and CPP associated with an antigen for disease, and introducing the antigen-associated CPP to (I), where antigen enters into the cell. The antigens are, for example, tumour antigen derived epitopes recognised by tumour infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I or II. The composition is useful for enhancing immunity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal, such that following the administration, animal is protected from disease, where the animal comprises both CD4+ and CD8+ T cells. It is also useful for treating a disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected to a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (I), preferably dendritic cell is prior to, subsequent to or concurrent with, the cancer treatment. The present sequence is a tumour antigen derived epitope for inclusion in the composition of the invention  
Sequence 15 AA;  
Query Match 100.0%; Score 83; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DYSYLQSDPDSFQD 15  
Db 1 DYSYLQSDPDSFQD 15  
RESULT 19  
ADA19544  
ID ADA19544 standard; peptide; 15 AA.  
AC ADA19544;  
DT 20-NOV-2003 (first entry)  
DE Human cancer antigen, tyrosinase (MHC HLA-DR4) #2.  
KW Lymphoid tissue-specific cell; haematopoietic progenitor cell; lymphoreticular stromal cell; transplantation; implantation; autoimmune disease; infectious disease; maintenance; expansion; differentiation; T cell tolerance; immune tolerance; T-cell reactivity; therapeutic; differentiated progeny; antigen; MHC; major histocompatibility complex; cancer; human.  
OS Homo sapiens.  
XX US6548299-B1.  
XX 15-APR-2003.  
XX 18-MAY-2000; 2000US-00574749.



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:34:47 ; Search time 42 Seconds  
(without alignments)  
100.478 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DYSYLQSDPDSPFQD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 199639

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	15	9	US-09-923-831-26
2	83	100.0	15	9	US-09-766-889A-38
3	83	100.0	15	12	US-10-218-095-33
4	83	100.0	15	14	US-10-161-097-25
5	83	100.0	15	14	US-10-170-832-67
6	70	84.3	13	9	US-09-847-185-42
7	70	84.3	13	14	US-10-224-286-42
8	70	84.3	13	15	US-10-406-317-14
9	70	84.3	13	15	US-10-676-309-30
10	70	84.3	13	16	US-10-297-168-14
11	34	41.0	14	12	US-10-103-395-72
12	33	39.8	10	9	US-09-962-055-22
13	33	39.8	10	9	US-09-976-740-22
14	33	39.8	10	12	US-10-671-242-22
15	33	39.8	10	13	US-10-023-529-22

16	33	39.8	10	13	US-10-023-523-22	Sequence 22, Appl
17	33	39.8	10	15	US-10-616-187-22	Sequence 22, Appl
18	31	37.3	13	9	US-09-732-411-2	Sequence 2, Appl
19	31	37.3	13	14	US-10-091-724-34	Sequence 34, Appl
20	31	37.3	13	15	US-10-431-048-34	Sequence 34, Appl
21	30	36.1	10	15	US-10-149-138-4326	Sequence 4326, Appl
22	29	34.9	9	12	US-10-398-104-50	Sequence 50, Appl
23	29	34.9	9	12	US-08-065-902-16	Sequence 16, Appl
24	29	34.9	11	12	US-10-398-104-190	Sequence 190, Appl
25	29	34.9	14	14	US-10-219-834-136	Sequence 136, Appl
26	28	33.7	7	10	US-08-847-946A-99	Sequence 99, Appl
27	28	33.7	8	10	US-08-847-946A-100	Sequence 100, Appl
28	28	33.7	9	8	US-08-344-824-157	Sequence 157, Appl
29	28	33.7	9	10	US-08-847-946A-91	Sequence 91, Appl
30	28	33.7	9	10	US-08-847-946A-94	Sequence 94, Appl
31	28	33.7	9	10	US-08-847-946A-97	Sequence 97, Appl
32	28	33.7	9	10	US-08-847-946A-98	Sequence 98, Appl
33	28	33.7	9	13	US-10-042-202-26	Sequence 26, Appl
34	28	33.7	9	14	US-10-219-850-20	Sequence 20, Appl
35	28	33.7	9	15	US-10-353-678-26	Sequence 26, Appl
36	28	33.7	10	10	US-08-847-946A-93	Sequence 93, Appl
37	28	33.7	10	10	US-08-847-946A-96	Sequence 96, Appl
38	28	33.7	11	10	US-08-847-946A-90	Sequence 90, Appl
39	28	33.7	12	10	US-09-992-665-5	Sequence 5, Appl
40	28	33.7	12	14	US-10-247-526-31	Sequence 31, Appl
41	28	33.7	12	14	US-10-251-526-31	Sequence 31, Appl
42	28	33.7	13	9	US-09-791-378-457	Sequence 457, Appl
43	28	33.7	15	9	US-09-894-018-275	Sequence 275, Appl
44	28	33.7	15	12	US-10-103-395-73	Sequence 73, Appl
45	28	33.7	15	12	US-10-103-395-241	Sequence 241, Appl

## ALIGNMENTS

RESULT 1  
US-09-923-831-26  
; Sequence 26, Application US/09923831  
; Patent No. US20020115142A1  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val,rie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/923,831  
; CURRENT FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 09/183,706  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 26  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-831-26

Query Match 100.0%; Score 83; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDSPFQD 15  
| | | | | | | | | | | | | | | |  
Db 1 DYSYLQSDPDSPFQD 15

RESULT 2  
US-09-766-889A-38  
; Sequence 38, Application US/09766889A  
; Patent No. US20020164654A1  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre



; APPLICANT: Strobant, Vincent  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: Schultz, Erwin  
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
; FILE REFERENCE: L0461/7104  
; CURRENT APPLICATION NUMBER: US/09/766,889A  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US 60/177,242  
; PRIOR FILING DATE: 2000-01-20  
; PRIOR APPLICATION NUMBER: US 60/243,212  
; PRIOR FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 38  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-766-889A-38

Query Match 100.0%; Score 83; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 3  
US-10-218-095-33  
; Sequence 33, Application US/10218095  
; Publication No. US20040033541A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Yi  
; APPLICANT: Strobant, Vincent  
; APPLICANT: Russo, Vincenzo  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF  
; FILE REFERENCE: L00461/70137  
; CURRENT APPLICATION NUMBER: US/10/218,095  
; CURRENT FILING DATE: 2002-08-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-218-095-33

Query Match 100.0%; Score 83; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 4  
US-10-161-097-25  
; Sequence 25, Application US/10161097  
; Publication No. US20030096404A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENZWEIG, Michael  
; APPLICANT: PVKETT, Mark J.  
; APPLICANT: SCADDEN, David T.  
; APPLICANT: POZNANSKI, Mark C.  
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
; TITLE OF INVENTION: DEVICES  
; FILE REFERENCE: C1005/7012/KM/ERG  
; CURRENT APPLICATION NUMBER: US/10/161,097

; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US/09/574,749  
; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/107,972  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: PCT/US99/26795  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/524,749  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Homo Sapiens source  
US-10-161-097-25

Query Match 100.0%; Score 83; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 5  
US-10-170-832-67  
; Sequence 67, Application US/10170832  
; Publication No. US20030170792A1  
; GENERAL INFORMATION:  
; APPLICANT: Chau, Pascal  
; APPLICANT: Vantomme, Valrie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Cortals, Jurgen  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/10/170,832  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US/09/166,448  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-832-67

Query Match 100.0%; Score 83; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15  
Db 1 DYSYLQSDPDPSFQD 15

RESULT 6  
US-09-847-185-42  
; Sequence 42, Application US/09847185  
; Patent No. US20020076392A1  
; GENERAL INFORMATION:  
; APPLICANT: Soo Hoo, William  
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; RESPONSE USING SAME  
; NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAMPBELL & FLORES, LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/847,185  
 FILING DATE: 01-May-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/201,931  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IM 2442  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)535-9001  
 TELEFAX: (619)535-8949  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
 US-09-847-185-42

Query Match 84.3%; Score 70; DB 9; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
 DB 1 SYLQSDPDPSFQD 13

RESULT 7  
 US-10-224-286-42  
 ; Sequence 42, Application US/10224286  
 ; Publication No. US20030108517A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soo Hoo, William  
 ; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 ; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 ; RESPONSE USING SAME  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CAMPBELL & FLORES, LLP  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 92121  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/224,286  
 ; FILING DATE: 19-Aug-2002  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/902,516  
 ; FILING DATE: 29-JUL-1997

Query Match 84.3%; Score 70; DB 15; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
 DB 1 SYLQSDPDPSFQD 13

RESULT 9  
 US-10-676-909-30  
 ; Sequence 30, Application US/10676909  
 ; Publication No. US20040086521A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KROPSHOFER, H.  
 ; APPLICANT: VOGT, A.  
 ; TITLE OF INVENTION: Method for the identification of antigenic peptides associated to

ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IM 2442  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)535-9001  
 TELEFAX: (619)535-8949  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
 US-10-224-286-42

Query Match 84.3%; Score 70; DB 14; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
 DB 1 SYLQSDPDPSFQD 13

RESULT 8  
 US-10-406-317-14  
 ; Sequence 14, Application US/10406317  
 ; Publication No. US20040019195A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlom, Jeffrey;  
 ; APPLICANT: Hodge, James;  
 ; APPLICANT: Panicali, Dennis  
 ; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
 ; TITLE OF INVENTION: molecules and uses thereof  
 ; FILE REFERENCE: 38163-0189  
 ; CURRENT APPLICATION NUMBER: US/10/406,317  
 ; CURRENT FILING DATE: 2003-04-04  
 ; PRIOR APPLICATION NUMBER: US/09/856,988  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/26866  
 ; PRIOR FILING DATE: 1999-11-12  
 ; PRIOR APPLICATION NUMBER: 60/111,582  
 ; PRIOR FILING DATE: 1998-12-09  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 14  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
 ; OTHER INFORMATION: PEPTIDE  
 US-10-406-317-14

Query Match 84.3%; Score 70; DB 9; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
 DB 1 SYLQSDPDPSFQD 13

RESULT 7  
 US-10-224-286-42  
 ; Sequence 42, Application US/10224286  
 ; Publication No. US20030108517A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soo Hoo, William  
 ; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 ; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 ; RESPONSE USING SAME  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CAMPBELL & FLORES, LLP  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 92121  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/224,286  
 ; FILING DATE: 19-Aug-2002  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/902,516  
 ; FILING DATE: 29-JUL-1997

Query Match 84.3%; Score 70; DB 15; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
 DB 1 SYLQSDPDPSFQD 13

RESULT 9  
 US-10-676-909-30  
 ; Sequence 30, Application US/10676909  
 ; Publication No. US20040086521A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KROPSHOFER, H.  
 ; APPLICANT: VOGT, A.  
 ; TITLE OF INVENTION: Method for the identification of antigenic peptides associated to

; FILE REFERENCE: 21388  
; CURRENT APPLICATION NUMBER: US/10/676,909  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: EP 0202223.8  
; PRIOR FILING DATE: 2002-02-10  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 30  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-676-909-30

Query Match 84.3%; Score 70; DB 16; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00032;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
| | | | | | | | | | | | |  
Db 1 SYLQSDPDPSFQD 13

RESULT 10  
US-10-297-168-14  
; Sequence 14, Application US/10297168  
; Publication No. US20040091995A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, Jeffrey  
; APPLICANT: GREINER, John W.  
; APPLICANT: KASS, Erik  
; APPLICANT: PANICALI, Dennis  
; TITLE OF INVENTION: RECOMBINANT NON-REPLICATING VIRUS EXPRESSING GM-CSF AND  
; FILE REFERENCE: 38163-0167  
; CURRENT APPLICATION NUMBER: US/10/297,168  
; PRIOR FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: PCT/US01/19201  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US60/211,717  
; PRIOR FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-297-168-14

Query Match 84.3%; Score 70; DB 16; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00032;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
| | | | | | | | | | | | |  
Db 1 SYLQSDPDPSFQD 13

RESULT 11  
US-10-103-395-72  
; Sequence 72, Application US/10103395  
; Publication No. US20020160019A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR  
; FILE REFERENCE: 39963-20016 01  
; CURRENT APPLICATION NUMBER: US/10/103,395  
; PRIOR FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: US 09/009,953  
; PRIOR FILING DATE: 1998-01-21

; PRIOR APPLICATION NUMBER: PCT/US98/01373  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: US 60/036,713  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: US 60/037,432  
; PRIOR FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 72  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-103-395-72

Query Match 41.0%; Score 34; DB 12; Length 14;  
Best Local Similarity 63.6%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 LQSDPDPSFQD 15  
| | | | | | | | | | | | |  
Db 4 LTDGIPDSIQD 14

RESULT 12  
US-09-962-055-22  
; Sequence 22, Application US/09962055  
; Patent No. US20020052033A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
; BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
; TREATING ATHEROSCLEROSIS  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/962,055  
; FILING DATE: 24-Sep-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/979,608  
; FILING DATE: 26-NOV-1997  
; APPLICATION NUMBER: US 60/031,930  
; FILING DATE: 27-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Louis  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-962-055-22

Query Match 39.8%; Score 33; DB 9; Length 10;

Best Local Similarity 62.5%; Pred. No. 1.1e+02; DB 9; Length 10;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 QSDPDPSF 13  
: |||||  
Db 1 EDDDPDGF 8

## RESULT 13

US-09-976-740-22  
; Sequence 22, Application US/09976740  
; Publication No. US20020194633A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/09/976,740  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 09/616,289  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-976-740-22

Query Match 39.8%; Score 33; DB 9; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 QSDPDPSF 13  
: |||||  
Db 1 EDDDPDGF 8

## RESULT 14

US-10-671-242-22  
; Sequence 22, Application US/10671242  
; Publication No. US20040040049A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/10/671,242  
; CURRENT FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: US/09/616,289  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/517,849  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-671-242-22

Query Match 39.8%; Score 33; DB 12; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 QSDPDPSF 13  
: |||||  
Db 1 EDDDPDGF 8

## RESULT 15

US-10-023-529-22  
; Sequence 22, Application US/10023529  
; Publication No. US20020129388A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/10/023,529  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 09/616,289  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/517,849  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-023-529-22

Query Match 39.8%; Score 33; DB 13; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 QSDPDPSF 13  
: |||||  
Db 1 EDDDPDGF 8

Search completed: June 3, 2004, 15:40:20  
Job time : 42 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 15:32:26 ; Search time 23 Seconds  
(without alignments)  
33.669 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83  
Sequence: 1 DYSYLQSDPDSPQD 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 146418

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

- Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	15	2	US-09-036-582-23
2	83	100.0	15	3	US-09-183-706-26
3	83	100.0	15	3	US-09-166-448-67
4	83	100.0	15	4	US-09-567-995-26
5	83	100.0	15	4	US-09-165-863-23
6	83	100.0	15	4	US-09-697-884-67
7	83	100.0	15	4	US-09-289-350-23
8	83	100.0	15	4	US-09-574-749B-25
9	83	100.0	15	4	US-09-118-141-23
10	83	100.0	15	4	US-09-169-717E-29
11	70	84.3	13	2	US-08-902-516-42
12	70	84.3	13	4	US-09-847-185-42
13	70	84.3	13	4	US-09-601-729-113
14	59	71.1	12	4	US-09-341-982-3
15	55	66.3	11	4	US-09-341-982-5
16	34	41.0	10	4	US-09-009-953-72
17	33	39.8	10	4	US-08-979-608A-22
18	33	39.8	10	4	US-09-517-849-22
19	33	39.8	10	4	US-09-616-289-22
20	31	37.3	15	1	US-08-520-977A-4
21	28	33.7	9	2	US-08-318-856A-59
22	28	33.7	12	4	US-09-462-118-31
23	28	33.7	12	4	US-09-009-953-73
24	28	33.7	15	4	US-09-009-953-73
25	28	33.7	15	4	US-09-311-784A-427
26	27.5	33.1	12	4	US-09-403-752A-46
27	27.5	33.1	14	1	US-08-165-301A-6

28 27.5 33.1 14 3 US-08-810-436-6  
29 27.5 33.1 14 5 PCT-US94-14179-6  
30 26 31.3 11 1 US-08-366-853A-4  
31 26 31.3 12 1 US-07-789-912-4  
32 26 31.3 12 4 US-09-632-627A-2  
33 26 31.3 13 4 US-09-386-962C-38  
34 26 31.3 14 2 US-08-466-860-40  
35 26 31.3 14 3 US-08-472-040A-40  
36 26 31.3 14 3 US-08-276-776-40  
37 26 31.3 14 3 US-08-471-209-40  
38 26 31.3 15 4 US-09-526-193A-49  
39 26 31.3 15 4 US-09-526-193A-50  
40 25 30.1 8 1 US-08-366-953A-13  
41 25 30.1 9 1 US-08-465-167A-35  
42 25 30.1 10 1 US-08-346-333-50  
43 25 30.1 10 1 US-08-465-167A-48  
44 25 30.1 10 4 US-09-535-852-1531  
45 25 30.1 10 5 PCT-US91-07506-50

## ALIGNMENTS

RESULT 1  
US-09-036-582-23  
; Sequence 23, Application US/09036582A  
; Patent No. 5965381  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Cornelis, Guy R.  
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
; TITLE OF INVENTION: WITH RECOMBINANT VERSINIA  
; FILE REFERENCE: 11154  
; CURRENT APPLICATION NUMBER: US/09/036,582A  
; CURRENT FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide  
US-09-036-582-23

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDSPQD 15  
DB 1 DYSYLQSDPDSPQD 15

RESULT 2  
US-09-183-706-26  
; Sequence 26, Application US/09183706  
; Patent No. 6245525  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/183,706  
; CURRENT FILING DATE: 1998-10-30  
; EARLIER APPLICATION NUMBER: 09/122,989  
; EARLIER FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 26  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-183-706-26

; Sequence 23, Application US/09289350

## RESULT 7

US-09-289-350-23  
; Sequence 23, Application US/09289350

```
/ Patent No. 6531451
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Durquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 11727Z
; CURRENT APPLICATION NUMBER: US/09/289,350
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Tyrosinase peptide
US-09-289-350-23

Query Match 100.0%; Score 83; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15
| | | | | | | | | | | | | | |
Db 1 DYSYLQSDPDPSFQD 15

RESULT 8
US-09-574-749B-25
; Sequence 25, Application US/09574749B
; Patent No. 6548299
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-25

Query Match 100.0%; Score 83; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15
| | | | | | | | | | | | | | |
```

```
Db 1 DYSYLQSDPDPSFQD 15

RESULT 9
US-09-318-141-23
; Sequence 23, Application US/09318141
; Patent No. 6602506
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy R.
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
; TITLE OF INVENTION: WITH RECOMBINANT YERSINIA
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/318,141
; CURRENT FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: US 09/036,582
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Tyrosinase peptide
US-09-318-141-23

Query Match 100.0%; Score 83; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15
| | | | | | | | | | | | | | |
Db 1 DYSYLQSDPDPSFQD 15

RESULT 10
US-09-169-717E-29
; Sequence 29, Application US/09169717E
; Patent No. 6667037
; GENERAL INFORMATION:
; APPLICANT: Ooms, Annie
; APPLICANT: Degiovanni, Gerard
; APPLICANT: Morel, Sandra
; APPLICANT: Van den Eynde, Benoit
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolater Peptides Which Bind To HLA-B35 Molecules,
; TITLE OF INVENTION: Larger Peptides Which Contain These, Nucleic Acid
; TITLE OF INVENTION: Molecules Encoding Peptides, And Uses Thereof
; FILE REFERENCE: LUD5561
; CURRENT APPLICATION NUMBER: US/09/169,717E
; CURRENT FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-169-717E-29

Query Match 100.0%; Score 83; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQSDPDPSFQD 15
| | | | | | | | | | | | | | |
Db 1 DYSYLQSDPDPSFQD 15

RESULT 11
US-08-902-516-42
; Sequence 42, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
```

;/ TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
;/ TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
;/ TITLE OF INVENTION: RESPONSE USING SAME  
;/ NUMBER OF SEQUENCES: 50  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSES: CAMPBELL & FLORES, LLP  
;/ STREET: 4370 La Jolla Village Drive, Suite 700  
;/ CITY: San Diego  
;/ STATE: California  
;/ COUNTRY: United States  
;/ ZIP: 92121  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/902,516  
;/ FILING DATE: 29-JUL-1997  
;/ CLASSIFICATION: 424  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Campbell, Cathryn A.  
;/ REGISTRATION NUMBER: 31,815  
;/ REFERENCE/DOCKET NUMBER: P-IM 2442  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (619)535-9001  
;/ TELEFAX: (619)535-8949  
;/ INFORMATION FOR SEQ ID NO: 42:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 13 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-902-516-42

Query Match 84.3%; Score 70; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
Db 1 SYLQSDPDPSFQD 13

RESULT 12  
US-09-847-185-42  
; Sequence 42, Application US/09847185  
; Patent No. 6482407  
; GENERAL INFORMATION:  
; APPLICANT: Soo Hoo, William  
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; RESPONSE USING SAME  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: CAMPBELL & FLORES, LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/847,185  
; FILING DATE: 01-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/201,931  
; FILING DATE: <Unknown>

;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Campbell, Cathryn A.  
;/ REGISTRATION NUMBER: 31,815  
;/ REFERENCE/DOCKET NUMBER: P-IM 2442  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (619)535-9001  
;/ TELEFAX: (619)535-8949  
;/ INFORMATION FOR SEQ ID NO: 42:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 13 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-09-847-185-42

Query Match 84.3%; Score 70; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
Db 1 SYLQSDPDPSFQD 13

RESULT 13  
US-09-601-729-113  
; Sequence 113, Application US/09601729  
; Patent No. 6683052  
; GENERAL INFORMATION:  
; APPLICANT: THIAM, KADER  
; APPLICANT: AURIAULT, CLAUDE  
; APPLICANT: GRAS-MASSE, HELENE  
; APPLICANT: LOING, ESTELLE  
; APPLICANT: VERWAERDE, CLAUDE  
; APPLICANT: GUILLET, JEAN GERARD  
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES  
; FILE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS  
; FILE REFERENCE: USB-97-AU-IN  
; CURRENT APPLICATION NUMBER: US/09/601,729  
; CURRENT FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: PCT/FR99/00259  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 98 01439  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 281  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 113  
; LENGTH: 13  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-601-729-113

Query Match 84.3%; Score 70; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYLQSDPDPSFQD 15  
Db 1 SYLQSDPDPSFQD 13

RESULT 14  
US-09-341-982-3  
; Sequence 3, Application US/09341982  
; Patent No. 6558671  
; GENERAL INFORMATION:  
; APPLICANT: SLINGLUFF, Craig L.  
; APPLICANT: HUNT, Donald F.  
; APPLICANT: ENGELHARD, Victor H.



; APPLICANT: KITTESEN, David  
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
; FILE REFERENCE: SLINGLUFF=3B  
; CURRENT APPLICATION NUMBER: US/09/341,982  
; EARLIER FILING DATE: 1999-09-20  
; EARLIER FILING DATE: 1998-01-29  
; EARLIER FILING DATE: 1997-01-31  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
; OTHER INFORMATION: human protein  
US-09-341-982-3

Query Match 71.1%; Score 59; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LQSDPDPSFQD 15  
| | | | | | | | | |  
Db 1 LQSDPDPSFQD 11

RESULT 15  
US-09-341-982-5  
; Sequence 5, Application US/09341982  
; Patent No. 6558671  
; GENERAL INFORMATION:  
; APPLICANT: SLINGLUFF, Craig L.  
; APPLICANT: HUNT, Donald F.  
; APPLICANT: ENGELHARD, Victor H.  
; APPLICANT: KITTESEN, David  
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
; FILE REFERENCE: SLINGLUFF=3B  
; CURRENT APPLICATION NUMBER: US/09/341,982  
; EARLIER FILING DATE: 1999-09-20  
; EARLIER FILING DATE: 1998-01-29  
; EARLIER FILING DATE: 1997-01-31  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
; OTHER INFORMATION: human protein  
US-09-341-982-5

Query Match 66.3%; Score 55; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0045;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QSDPDPSFQD 15  
| | | | | | | | | |  
Db 1 QSDPDPSFQD 10

Search completed: June 3, 2004, 15:35:51  
Job time : 23 secs